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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 84.1064 Seconds

(without alignments)  
1843.986 Million cell updates/sec

Title: US-09-389-782A-2

Perfect score: 2179  
Sequence: 1 MNKWCCALLVLLDIEWT.....QKLFLEMIGNQVSKISCL 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2179	100.0	401	2 AAW38344	Aaw38344 Mouse ost
2	2179	100.0	401	4 AAB80898	Aab80898 Human ost
3	2179	100.0	401	4 AAY72916	Aay72916 Human ost
4	2179	100.0	401	4 AAB66975	Aab66975 Murine OP
5	2179	100.0	401	8 ADM28811	Adm28811 Mouse ost
6	2079	95.4	401	2 AAW38343	Aaw38343 Rat osteo
7	2079	95.4	401	4 AAB66974	Aab66974 Rat OPG.
8	2079	95.4	401	8 ADM28809	Adm28809 Rat osteo
9	2061	94.6	380	4 AAB66987	Aab66987 Human OPG
10	2061	94.6	380	8 ADM28826	Adm28826 Mouse ost
11	2050	94.1	380	8 ADM28861	Adm28861 Mouse ost
12	1900	87.2	401	2 AAY05742	Aay05742 Tumour ne
13	1900	87.2	401	2 AAW95030	Aaw95030 Tumour ne
14	1900	87.2	401	2 AAW83926	Aaw83926 Human FTH
15	1900	87.2	401	3 AAB18715	Aab18715 A human t
16	1900	87.2	401	4 AAB60570	Aab60570 Human TNF
17	1900	87.2	401	6 AAB36245	Aab36245 Human TRA
18	1900	87.2	401	6 AAO31135	Aao31135 Human TRA
19	1900	87.2	401	7 ADD01625	Add01625 Human ost
20	1900	87.2	401	7 ADF16158	Adf16158 Human alb
21	1900	87.2	401	7 ADF16153	Adf16153 Human alb
22	1900	87.2	401	7 ADF16151	Adf16151 Human alb
23	1900	87.2	401	7 ADF15231	Adf15231 Human alb
24	1900	87.2	401	7 ADF16152	Adf16152 Human alb
25	1900	87.2	401	7 ADF16154	Adf16154 Human alb

26	1900	87.2	401	7 ADF16155	Adf16155 Human alb
27	1900	87.2	401	7 ADF16156	Adf16156 Human alb
28	1900	87.2	401	7 ADF15230	Adf15230 Human alb
29	1900	87.2	401	7 ADF15244	Adf15244 Human alb
30	1900	87.2	401	7 ADF16157	Adf16157 Human alb
31	1900	87.2	401	8 ADK82154	Adk82154 Human TRA
32	1900	87.2	986	7 ADF15016	Adf15016 Human alb
33	1900	87.2	986	7 ADF15030	Adf15030 Human alb
34	1895	87.0	401	2 AAW99925	Aaw99925 Full leng
35	1895	87.0	401	2 AAW53239	Aaw53239 Human OCI
36	1895	87.0	401	3 AAY88622	Aay88622 Osteoclas
37	1895	87.0	401	6 ABP70997	Abp70997 Human ost
38	1895	87.0	401	7 ADD37427	Add37427 Human ost
39	1895	87.0	401	8 ADQ68056	Adq68056 Human ost
40	1892	86.8	401	2 AAW38345	Aaw38345 Human ost
41	1892	86.8	401	3 AAY43400	Aay43400 Osteoprot
42	1892	86.8	401	4 AAB66976	Aab66976 Human OPG
43	1892	86.8	401	5 ABG71823	Abg71823 Wild type
44	1892	86.8	401	6 ABP55109	Abp55109 Human ost
45	1892	86.8	401	6 AAE34363	Aae34363 Human ost

ALIGNMENTS

RESULT 1  
AAW38344  
ID AAW38344 standard; protein; 401 AA.

XX AAW38344;

XX 20-APR-1998 (first entry)

XX Mouse osteoprotegerin.

XX Osteoprotegerin; antibody; diagnosis; affinity purification;  
KW recombinant production; transgenic animal; treatment; prevention;  
KW antisense oligonucleotide; probe; detection; screening; mouse;  
KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;  
KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;  
KW osteolytic metastasis; periodontal bone loss; bone necrosis; osteopaenia;  
KW murine.

XX Mus sp.

XX Key Location/Qualifiers  
FT CDS 90..1295  
FT /tag=a  
FT /product="osteoprotegerin"

FT DE19654610-A1.

PD 26-JUN-1997.

XX 20-DEC-1996; 96DE-01054610.

XX 22-DEC-1995; 95US-00577788.

PR 03-SEP-1996; 96US-00706945.

XX (AMGE-) AMGEN INC.

PA Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX WPI; 1997-334271/31.

DR N-PSDB; AAT96062.

XX Nucleic acid encoding osteoprotegerin - useful for treatment of diseases

PT involving excessive bone loss, e.g. osteoporosis.

XX Claim 23; Page 106-107; 182pp; German.

XX The present sequence is mouse osteoprotegerin (OPG). Anti-OPG antibodies

CC can be used in OPG diagnostic assays, and as affinity purification

CC materials. The OPG cDNA can be used to express recombinant OPG and to  
 CC generate transgenic animals. It can also be used to regulate the level of  
 CC OPG in mammals, specifically to increase OPG levels, however the use of  
 CC antisense sequences is also contemplated. Fragments of the cDNA can be  
 CC used as probes to detect OPG expressing cells and tissue, and to screen  
 CC cDNA libraries for related sequences. OPG can be used to treat or prevent  
 CC bone diseases, specifically excessive bone loss, e.g. osteoporosis,  
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid  
 CC arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,  
 CC bone necrosis and osteopaenia

XX Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 2; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-174;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTQETLPPKYLHYDPETHQLLCDKCAPGYLKHQCTVRRKT 60  
 DB 1 MNKWLCCALLVLLDIIETWTQETLPPKYLHYDPETHQLLCDKCAPGYLKHQCTVRRKT 60

QY 61 LCVPCPDHSYDTSWHTSDVCVCSVKELQSVQECNRTNHRVCEBEGRYLEIEFCLK 120  
 DB 61 LCVPCPDHSYDTSWHTSDVCVCSVKELQSVQECNRTNHRVCEBEGRYLEIEFCLK 120

QY 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGSETSSKAPCIKHTNCSFTGLLIQKGNAT 180  
 DB 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGSETSSKAPCIKHTNCSFTGLLIQKGNAT 180

QY 181 HDNVCSGNREATQKCGIDVTLCCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240  
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240

QY 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIQQIDLCSSVQRHGHNSNLTEQLLALME 300  
 DB 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIQQIDLCSSVQRHGHNSNLTEQLLALME 300

QY 301 SLPGKKISPEIERTRKTKCSSEQLKLLSLWRINKGQDQTLKGLMYALKHLKTSHPFKT 360  
 DB 301 SLPGKKISPEIERTRKTKCSSEQLKLLSLWRINKGQDQTLKGLMYALKHLKTSHPFKT 360

QY 361 VTHSLRKTMRFHLSMTVRLYQKLFLEMIGNQVSKISCL 401  
 DB 361 VTHSLRKTMRFHLSMTVRLYQKLFLEMIGNQVSKISCL 401

# RESULT 2

AAB80898 standard; protein; 401 AA.

XX AAB80898;

XX 31-MAY-2001 (first entry)

XX Human osteoprotegrin, OPG.

XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;  
 KW osteoclast formation inhibition; bone resorption inhibition.

XX Homo sapiens.

XX WO200117543-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.

XX (AMGE-) AMGEN INC.

XX Dunstan CR;

XX WPI; 2001-265936/27.

XX Preventing or treating lytic bone diseases, particularly associated with  
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.

XX Claim 5; Fig 2; 87pp; English.

CC The present invention relates to a method for the prevention or treatment  
 CC of lytic bone disease or multiple myeloma. Also the method can be used  
 CC for preventing metastasis of cancer to bone or osteosclerotic bone  
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)  
 CC polypeptide or OPG fusion protein (see AAB80899-AAB80904). The present  
 CC sequence is human OPG. OPG inhibits formation of osteoclasts (and thus  
 CC bone resorption) by blocking differentiation from monocytes/macrophage  
 CC precursors. The OPG polypeptide can be used in a method of preventing or  
 CC treating lytic bone disease, for preventing metastasis of cancer to bone  
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal  
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic  
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
 CC or treatment of loss of bone mass, which occurs in conditions including  
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic lupus erythematosus and other conditions; bone  
 CC cell anaemia, systemic necrosis associated with Gaucher's disease; sickle  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
 CC metastases

XX Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 4; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-174;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTQETLPPKYLHYDPETHQLLCDKCAPGYLKHQCTVRRKT 60  
 DB 1 MNKWLCCALLVLLDIIETWTQETLPPKYLHYDPETHQLLCDKCAPGYLKHQCTVRRKT 60

QY 61 LCVPCPDHSYDTSWHTSDVCVCSVKELQSVQECNRTNHRVCEBEGRYLEIEFCLK 120  
 DB 61 LCVPCPDHSYDTSWHTSDVCVCSVKELQSVQECNRTNHRVCEBEGRYLEIEFCLK 120

QY 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGSETSSKAPCIKHTNCSFTGLLIQKGNAT 180  
 DB 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGSETSSKAPCIKHTNCSFTGLLIQKGNAT 180

QY 181 HDNVCSGNREATQKCGIDVTLCCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240  
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFRRFAVPTKIIPNWLSVLDSPGTVKNAESVERI 240

QY 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIQQIDLCSSVQRHGHNSNLTEQLLALME 300  
 DB 241 KRRHSSQEQTFOLLKWKHQRNDQEMVKKIQQIDLCSSVQRHGHNSNLTEQLLALME 300

QY 301 SLPGKKISPEIERTRKTKCSSEQLKLLSLWRINKGQDQTLKGLMYALKHLKTSHPFKT 360  
 DB 301 SLPGKKISPEIERTRKTKCSSEQLKLLSLWRINKGQDQTLKGLMYALKHLKTSHPFKT 360

Db 301 SLPGKKISPEEIERTRKTKSSBQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPKPT 360

QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 3

AAY72916

ID AAY72916 standard; protein; 401 AA.

XX

AC AAY72916;

DT 13-JUN-2001 (first entry)

XX

DE Human osteoprotegerin (OPG).

XX

KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;

KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;

KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;

KW periodontal.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..21

FT /label= Signal\_peptide

FT Protein 22..401

FT /label= Mature\_osteoprotegerin

XX

PN WO200118203-A1.

XX

PD 15-MAR-2001.

XX

PF 18-AUG-2000; 2000WO-US022797.

XX

PR 03-SEP-1999; 99US-00389782.

XX

PA (AMGE-) AMGEN INC.

XX

PI Dunstan CR, Wooden SK, Mann MB;

XX

DR WPI; 2001-244572/25.

XX

PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused

PT by e.g. osteoporosis, Paget's disease and osteomyelitis.

XX

PS Claim 4; Fig 2; 119pp; English.

XX

CC The present sequence is human osteoprotegerin (OPG) protein. This

CC sequence is fused with the Fc region of human immunoglobulin G1 (IgG1) by

CC a linker sequence to form a fusion protein. OPG negatively regulates the

CC formation of osteoclasts in vitro and in vivo. It blocks the

CC differentiation of osteoclasts from monocyte or macrophage precursors and

CC the reabsorption of bone. The OPG-Fc fusion protein is administered for

CC the treatment of bone loss resulting from osteoporosis, Paget's disease,

CC osteomyelitis, hypercalcaemia, osteopenia associated with surgery or

CC steroid administration, osteonecrosis, bone loss due to rheumatoid

CC arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic

CC loosening

XX

SQ Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 4; Length 401;

Best Local Similarity 100.0%; Pred. No. 2.6e-174;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKT 60

Db 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKT 60

QY 61 LCVPCPDHSYTDSWHTSDECVYCSVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120

Db 61 LCVPCPDHSYTDSWHTSDECVYCSVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120

QY 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFSGSETSKAPCIKHITNCSTFGLLLIQKNAT 180

Db 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFSGSETSKAPCIKHITNCSTFGLLLIQKNAT 180

QY 181 HDNVCSGNREATQKCGIDVTLCCEAFAFPAPVTKIIPNWLVLVDLSPGTVKNAESVERI 240

Db 181 HDNVCSGNREATQKCGIDVTLCCEAFAFPAPVTKIIPNWLVLVDLSPGTVKNAESVERI 240

QY 241 KRRHSSQEQTFOLLKLWKHQRDQEMVKIIQDIDLCESSVORHLGHSNLTTEQLLAME 300

Db 241 KRRHSSQEQTFOLLKLWKHQRDQEMVKIIQDIDLCESSVORHLGHSNLTTEQLLAME 300

QY 301 SLPGKKISPEEIERTRKTKSSEQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPKPT 360

Db 301 SLPGKKISPEEIERTRKTKSSEQLKLLSLWRIKNGDQDTLKLGLMYALKHLKTSHPKPT 360

QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 4

AAB66975

ID AAB66975 standard; protein; 401 AA.

XX

AC AAB66975;

DT 19-APR-2001 (first entry)

XX

DE Murine OPG.

XX

KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;

KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;

KW systemic lupus erythematosus; graft-versus-host disease; septic shock;

KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;

KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;

KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;

KW ischaemia; Parkinson's disease.

XX

OS Mus sp.

XX

PN WO200103719-A2.

XX

PD 18-JAN-2001.

XX

PF 07-JUL-2000; 2000WO-US018667.

XX

PR 09-JUL-1999; 99US-00350670.

PR 09-DEC-1999; 99US-00457647.

XX

PA (AMGE-) AMGEN INC.

XX

PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX

DR WPI; 2001-103031/11.

DR N-PSDB; AAF57837.

XX

PT Treating conditions leading to bone loss such as rheumatoid arthritis,

PT multiple sclerosis and asthma, comprises administering an osteoprotegerin

PT protein in conjunction with e.g. inhibitors of interleukin and tumor

PT necrosis factor alpha.

XX

PS Example 5; Fig 9; 316pp; English.

XX

CC The present invention relates to a method for treating conditions leading

CC to bone loss. The method comprises administering a purified and isolated

CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)

CC in conjunction with other substances such as tumour necrosis factor-alpha

CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE

CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet

activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock

Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 2.6e-174;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIETWTQETLPKYLHYDPETHQLLCDKAPGTYLKQCTVRRKT 60  
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Db 241 KRHSSEQTFOILLKWKHQNDRQEMVKIIQIDILCESSVORHLGHSNLTTEQLALME 300

QY 301 SLPGKKISPEETERTKTKCSSEQLLKLWLRIKNGDQDTLKLGLMYALKHLKTSHPFKT 360  
Db 301 SLPGKKISPEETERTKTKCSSEQLLKLWLRIKNGDQDTLKLGLMYALKHLKTSHPFKT 360

QY 361 VTHSLRKTRWFLHSFTMYRLYOKLFLEMTGNQVQSVKISCL 401  
Db 361 VTHSLRKTRWFLHSFTMYRLYOKLFLEMTGNQVQSVKISCL 401

RESULT 5  
ADM28811  
ID ADM28811 standard; protein; 401 AA.  
XX  
AC ADM28811;  
DT 20-MAY-2004 (first entry)  
XX  
DE Mouse osteoprotegerin, OPG.  
XX  
KW Mouse; OPG; bone resorption; excessive bone loss; osteoporosis;  
KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;  
KW steroid-induced osteopenia; rheumatoid arthritis; osteomyelitis;  
KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;  
KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;  
KW Riley-day syndrome; immobilisation of extremity; tumour;  
KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;  
KW renal function disorder; osteopenia; osteonecrosis; bone cell death;  
KW osteoprotegerin; transgenic.  
OS Mus sp.  
FH Location/Qualifiers  
FT 1..21  
FT /note= "Signal peptide"  
FT 22..401  
FT /note= "Mature OPG"

FT Region 22..201  
FT /note= "Claimed in claim 32"  
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FT Region 22..189  
FT /note= "Claimed in claim 32"  
FT Region 22..185  
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FT Region 27..401  
FT /note= "Claimed in claim 35"  
FT Region 27..194  
FT /note= "Claimed in claim 35"  
FT Region 27..189  
FT /note= "Claimed in claim 35"  
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FT /note= "Claimed in claim 35"  
FT Region 32..401  
FT /note= "Claimed in claim 35"  
US2003207827-A1.  
PD 06-NOV-2003.  
XX 24-SEP-1999; 99US-00405032.  
XX 22-DEC-1995; 95US-00577788.  
PR 03-SEP-1996; 96US-00706945.  
PR 20-DEC-1996; 96US-00771777.  
PR 12-AUG-1998; 98US-00132985.  
XX (BOYL/) BOYLE W J.  
PA (LACE/) LACEY D L.  
PA (CALZ/) CALZONE F J.  
XX (CHAN/) CHANG M.  
PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;  
XX WPI; 2004-041572/04.  
DR N-PSDB; ADM28810.  
XX  
PT Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis.  
XX Claim 23; SEQ ID NO 123; 141pp; English.  
XX  
CC The invention relates to a purified and isolated polypeptide having osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or having amino terminus at residue 22, and 1-216 amino acids are deleted from carboxy terminus of human OPG polypeptide. Also included are an isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression vector comprising OPG NA, a host cell transformed or transfected with the polypeptide comprising an amino acid sequence of at least about 164 amino acids comprising four cysteine-rich domains characteristic of the cysteine rich domains of tumour necrosis factor receptor extracellular regions (and an activity of increasing bone density), an antibody (Ab) or its fragment which specifically binds to OPG, a composition comprising OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) and an osteoprotegerin multimer consisting of osteoprotegerin monomers. Ab is useful for detecting the presence of OPG in a biological sample which involves incubating the sample with Ab under conditions that allow binding of Ab to OPG and detecting the bound Ab. OPG is useful for assessing the ability of a candidate substance to bind to OPG. OPG NA is useful for regulating the levels of OPG in an animal (human). The nucleic acid promotes an increasing in tissue level of OPG. OPG is useful for treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced osteopenia, bone loss due to rheumatoid arthritis, bone loss due to osteomyelitis, osteolytic metastasis, and periodontal bone loss. The method further involves administering a substance chosen from bone morphogenic protein BMP-1 through BMP-12, TGF-beta family members, Il-1 inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,

CC parathyroid hormone related protein and their analogues, B series; of  
 CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is  
 CC useful for treating osteoporosis such as primary osteoporosis, endocrine  
 CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),  
 CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta  
 CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and  
 CC osteoporosis due to immobilisation of extremities, hypercalcaemia  
 CC resulting from solid tumours and haematologic malignancies (multiple  
 CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and  
 CC hypercalcaemia associated with hyperthyroidism and renal function.  
 CC disorders, osteopaenia following surgery and osteonecrosis or bone cell  
 CC death. The present sequences is an OPG protein (or fragment).  
 XX  
 SQ Sequence 401 AA;

Query Match 100.0%; Score 2179; DB 8; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-174;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKAPGTYLKQHCIVRRKT 60  
 DB 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKAPGTYLKQHCIVRRKT 60  
 QY 61 LCVPCPDHSYTDSTWHTSDCVYCSVPCKELQSVKQECNTHNRVCEEGRYLEIFCLK 120  
 DB 61 LCVPCPDHSYTDSTWHTSDCVYCSVPCKELQSVKQECNTHNRVCEEGRYLEIFCLK 120  
 QY 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
 DB 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIPNWLSDLVSLPGTKVNAESVERI 240  
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIPNWLSDLVSLPGTKVNAESVERI 240  
 QY 241 KRRHSSQEQTFOLLKWKHQNDRQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
 DB 241 KRRHSSQEQTFOLLKWKHQNDRQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
 QY 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDODTLKGLMYALKHLKTSHPFKT 360  
 DB 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDODTLKGLMYALKHLKTSHPFKT 360  
 QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401  
 DB 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401

RESULT 6  
 AAW38343  
 ID AAW38343 standard; protein; 401 AA.  
 XX  
 AC AAW38343;  
 XX  
 DT 20-APR-1998 (first entry)  
 XX  
 DE Rat osteoprotegerin.  
 XX  
 KW Rat; osteoprotegerin; antibody; diagnosis; diagnosis; affinity purification;  
 KW recombinant production; transgenic animal; treatment; prevention;  
 KW antisense oligonucleotide; probe; detection; screening; bone disease;  
 KW osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;  
 KW rheumatoid arthritis; osteomyelitis; osteolytic metastases;  
 KW periodontal bone loss; bone necrosis; osteopaenia.  
 XX  
 OS Rattus sp.  
 XX  
 PN DE19654610-A1.  
 XX  
 PD 26-JUN-1997.  
 XX  
 XX 20-DEC-1996; 96DE-01054610.  
 XX

PR 22-DEC-1995; 95US-00577788.  
 PR 03-SEP-1996; 96US-00706945.  
 XX (AMGE-) AMGEN INC.  
 XX Boyle WJ, Lacey DL, Calzone FJ, Chang M;  
 XX WPI; 1997-334271/31.  
 DR N-PSDB; AAT96061.  
 XX  
 XX Nucleic acid encoding osteoprotegerin - useful for treatment of diseases  
 PT involving excessive bone loss, e.g. osteoporosis.  
 XX  
 PS Claim 23; Page 102-104; 182pp; German.  
 XX  
 CC The present sequence is rat osteoprotegerin (OPG). Anti-OPG antibodies  
 CC can be used in OPG diagnostic assays, and as affinity purification  
 CC materials. The OPG cDNA can be used to express recombinant OPG and to  
 CC generate transgenic animals. It can also be used to regulate the level of  
 CC OPG in mammals, specifically to increase OPG levels, however the level of  
 CC antisense sequences is also contemplated. Fragments of the cDNA can be  
 CC used as probes to detect OPG expressing cells and tissue, and to screen  
 CC cDNA libraries for related sequences. OPG can be used to treat or prevent  
 CC bone diseases, specifically excessive bone loss, e.g. osteoporosis,  
 CC Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid  
 CC arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,  
 CC bone necrosis and osteopaenia  
 XX  
 SQ Sequence 401 AA;

Query Match 95.4%; Score 2079; DB 2; Length 401;  
 Best Local Similarity 94.5%; Pred. No. 6.5e-166;  
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKAPGTYLKQHCIVRRKT 60  
 DB 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKAPGTYLKQHCIVRRKT 60  
 QY 61 LCVPCPDHSYTDSTWHTSDCVYCSVPCKELQSVKQECNTHNRVCEEGRYLEIFCLK 120  
 DB 61 LCVPCPDHSYTDSTWHTSDCVYCSVPCKELQSVKQECNTHNRVCEEGRYLEIFCLK 120  
 QY 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
 DB 121 HRSCPPGSGVQAGTPERNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIPNWLSDLVSLPGTKVNAESVERI 240  
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFFRFAVPTKIIPNWLSDLVSLPGTKVNAESVERI 240  
 QY 241 KRRHSSQEQTFOLLKWKHQNDRQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
 DB 241 KRRHSSQEQTFOLLKWKHQNDRQEMVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
 QY 301 SLPGKKISPEEIERTRKTKCSSEQLLKLWLRIKNGDODTLKGLMYALKHLKTSHPFKT 360  
 DB 301 SLPGKKISPEEIERTRKTKCPSEQLLKLWLRIKNGDODTLKGLMYALKHLKTSHPFKT 360  
 QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401  
 DB 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401

RESULT 7  
 AAB66974  
 ID AAB66974 standard; protein; 401 AA.  
 XX  
 AC AAB66974;  
 XX  
 DT 19-APR-2001 (first entry)  
 XX  
 XX Rat OPG.  
 XX



XX PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;  
XX WPI; 2004-041572/04.  
DR N-PSDB; ADM28808.  
DR PT Novel osteoprotegerin useful for treating conditions resulting in bone  
PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone  
PT loss caused by rheumatoid arthritis or osteomyelitis.  
XX Claim 23; SEQ ID NO 121; 141pp; English.  
XX The invention relates to a purified and isolated polypeptide having  
CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or  
CC having amino terminus at residue 22, and 1-216 amino acids are deleted  
CC from carboxy terminus of human OPG polypeptide. Also included are an  
CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression  
CC vector comprising OPG NA, a host cell transformed or transfected with the  
CC vector, a transgenic mammal comprising the cell, producing OPG, a  
CC polypeptide comprising an amino acid sequence of at least about 164 amino  
CC acids comprising four cysteine-rich domains characteristic of the  
CC cysteine rich domains of tumour necrosis factor receptor extracellular  
CC regions (and an activity of increasing bone density), an antibody (Ab) or  
CC its fragment which specifically binds to OPG, a composition comprising  
CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)  
CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.  
CC Ab is useful for detecting the presence of OPG in a biological sample  
CC which involves incubating the sample with Ab under conditions that allow  
CC binding of Ab to OPG and detecting the bound Ab. OPG is useful for  
CC assessing the ability of a candidate substance to bind to OPG. OPG NA is  
CC useful for regulating the levels of OPG in an animal (human). The nucleic  
CC acid promotes an increasing in tissue level of OPG. OPG is useful for  
CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's  
CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced  
CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to  
CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The  
CC method further involves administering a substance chosen from bone  
CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1  
CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,  
CC parathyroid hormone related protein and their analogues, E series of  
CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is  
CC useful for treating osteoporosis such as primary osteoporosis, endocrine  
CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),  
CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta  
CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and  
CC osteoporosis due to immobilisation of extremities, hypercalcaemia  
CC resulting from solid tumours and haematologic malignancies (multiple  
CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and  
CC hypercalcaemia associated with hyperthyroidism and renal function  
CC disorders, osteopaenia following surgery and osteonecrosis or bone cell  
CC death. The present sequences is an OPG protein (or fragment).  
XX SQ Sequence 401 AA;  
  
Query Match 95.4%; Score 2079; DB 8; Length 401;  
Best Local Similarity 94.5%; Pred. No. 6.5e-166;  
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 MNKWLCCALLVLDIIETWTQETLPKYLHYDPTGQHLCDKCAPCTYLVKHCTVRRKT 60  
Db 1 MNKWLCCALLVLDIIETWTQETFPFKYLHYDPTGQHLCDKCAPCTYLVKHCTVRRKT 60  
  
QY 61 LCVPFCDHSYTDWSHTSDSCVSPVKELQSVKQECNTRHNRCVCEGRYLEIFBCLK 120  
Db 61 LCVPFCDYSYTDWSHTSDSCVSPVKELQTVKQECNTRHNRCVCEGRYLEIFBCLK 120  
  
QY 121 HRCSPGSGVQAGTPTERNVTCKPDGPFSGTSSKAPCIKTNCTSTFGLLIQKGNAT 180  
Db 121 HRCSPGGLVQAGTPTERNVTCKPDGPFSGTSSKAPCKRHTNCSLLGLLIQKGNAT 180  
  
QY 181 HDNVCSGNREATCKGIDVTLCBEAFRFAVPTKIIIPNVLVDSIPGCKVNAESVERI 240  
Db 181 HDNVCSGNREATQCGIDVTLCBEAFRFAVPTKIIIPNVLVDSIPGCKVNAESVERI 240

QY 241 KRRHSQEQTFOLLKWLKQHNDRQENVKKIIQIDILCESSVQRHLGHSNLTTFQLALME 300  
Db 241 KRRHSQEQTFOLLKWLKQHNDRQENVKKIIQIDILCESSVQRHLGHSNLTTFQLALME 300  
  
QY 301 SLPGKKISPEETERTKTKCSFOLLKLLSLWRIKNGDDDTLKLGMVYALKHLKLTSHPPKT 360  
Db 301 SLPGKKISPEETERTKTKCPSEQLKLLSLWRIKNGDDDTLKLGMVYALKHLKLTSHPPKT 360  
  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
  
RESULT 9  
AAB66987  
ID AAB66987 standard; protein; 380 AA.  
XX AAB66987;  
AC AAB66987;  
XX 19-APR-2001 (first entry)  
DT Human OPG cysteine-rich domain.  
XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
KW ischaemia; Parkinson's disease.  
XX Homo sapiens.  
OS WO200103719-A2.  
XX 18-JAN-2001.  
PD 07-JUL-2000; 2000WO-US018667.  
XX 09-JUL-1999; 99US-00350670.  
PR 09-DEC-1999; 99US-00457647.  
XX (AMGS-) AMGEN INC.  
PA Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;  
WPI; 2001-103031/11.  
XX Treating conditions leading to bone loss such as rheumatoid arthritis,  
PT multiple sclerosis and asthma, comprises administering an osteoprotegerin  
PT protein in conjunction with e.g. inhibitors of interleukin and tumor  
PT necrosis factor alpha.  
XX Disclosure; Fig 12; 316pp; English.  
PS The present invention relates to a method for treating conditions leading  
XX to bone loss. The method comprises administering a purified and isolated  
CC osteoprotegerin (OPG) protein (AAPS7836-AAPS7838 and AAB66974-AAB66976)  
CC in conjunction with other substances such as tumour necrosis factor-alpha  
CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
CC modulating, fibroblast growth factor (FGF)1-10 modulators and/or platelet  
CC activating factor (PAF) antagonists. The method is useful for treating  
CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
CC graft-versus-host disease (GVHD). Other diseases that can be treated  
CC include acute pancreatitis, Alzheimer's disease, anorexia,  
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
CC psoriasis and septic shock  
XX

SQ Sequence 380 AA;

Query Match 94.6%; Score 2061; DB 4; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 2e-164;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 ETLPPKYLHYDPETGHQLCDKCAPGYLKQCHTVRRKTLVCPDHSYDTSWHTSDECV 81  
 Db 1 ETLPPKYLHYDPETGHQLCDKCAPGYLKQCHTVRRKTLVCPDHSYDTSWHTSDECV 60

Qy 82 YCSVCKELQSVKQECNRTNHRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERTNV 141  
 Db 61 YCSVCKELQSVKQECNRTNHRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERTNV 120

Qy 142 CKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATHDNCVSGNREATQKCGIDVTL 201  
 Db 121 CKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATHDNCVSGNREATQKCGIDVTL 180

Qy 202 CEEAFFRFAVPTKIIIPNWLVSVDLPSTGTVKNAESVERIKRRHSSQEQTFQLLKLWKHQ 261  
 Db 181 CEEAFFRFAVPTKIIIPNWLVSVDLPSTGTVKNAESVERIKRRHSSQEQTFQLLKLWKHQ 240

Qy 262 RDEMWVKIIQDIDLCESSVQRHLGSHNLTEQLLALMESLPCKISPEIERTRTKCS 321  
 Db 241 RDEMWVKIIQDIDLCESSVQRHLGSHNLTEQLLALMESLPCKISPEIERTRTKCS 300

Qy 322 SEQLKLLSLWRIRKNGDQDTLKGIMVALKHLKTSHPFKVTTHSLRKTMRFLHSFTMYRL 381  
 Db 301 SEQLKLLSLWRIRKNGDQDTLKGIMVALKHLKTSHPFKVTTHSLRKTMRFLHSFTMYRL 360

Qy 382 OKLFLEMGVQSVKISCL 401  
 Db 361 OKLFLEMGVQSVKISCL 380

RESULT 10  
 ADM28826  
 ID ADM28826 standard; protein; 380 AA.  
 AC ADM28826;  
 XX  
 DT 20-MAY-2004 (first entry)  
 DE Mouse osteoprotegerin cysteine-rich domains 1-4 plus C-terminus #1.  
 KW Mouse; OPG; bone resorption; excessive bone loss; osteoporosis;  
 KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;  
 KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;  
 KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;  
 KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;  
 KW Riley-day syndrome; immobilisation of extremity; tumour;  
 KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;  
 KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;  
 KW osteoprotegerin; transgenic.  
 XX  
 OS Mus sp.  
 XX  
 XX US2003207827-A1.  
 PN  
 XX  
 XX 06-NOV-2003.  
 PD  
 XX  
 XX 24-SEP-1999; 99US-00405032.  
 XX  
 XX 22-DEC-1995; 95US-00577788.  
 PR  
 PR 03-SEP-1996; 96US-00706945.  
 PR 20-DEC-1996; 96US-00771777.  
 PR 12-AUG-1998; 98US-00132985.  
 XX  
 PA (BOYL/) BOYLE W J.  
 PA (LACE/) LACEY D L.  
 PA (CALZ/) CALZONE F J.  
 PA (CHAN/) CHANG M.  
 XX

PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;  
 XX WPI; 2004-041572/04.  
 XX  
 PT Novel osteoprotegerin useful for treating conditions resulting in bone  
 loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone  
 loss caused by rheumatoid arthritis or osteomyelitis.  
 PT  
 XX  
 PS Disclosure; SEQ ID NO 138; 141pp; English.  
 XX  
 CC The invention relates to a purified and isolated polypeptide having  
 osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or  
 having amino terminus at residue 22, and 1-216 amino acids are deleted  
 from carboxy terminus of human OPG polypeptide. Also included are an  
 isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression  
 vector comprising OPG NA, a host cell transformed or transfected with the  
 vector, a transgenic mammal comprising the cell, producing OPG, a  
 polypeptide comprising an amino acid sequence of at least about 164 amino  
 acids comprising four cysteine-rich domains characteristic of the  
 cysteine rich domains of tumour necrosis factor receptor extracellular  
 regions (and an activity of increasing bone density), an antibody (Ab) or  
 its fragment which specifically binds to OPG, a composition comprising  
 OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)  
 and an osteoprotegerin multimer consisting of osteoprotegerin monomers.  
 CC Ab is useful for detecting the presence of OPG in a biological sample  
 which involves incubating the sample with Ab under conditions that allow  
 binding of Ab to OPG and detecting the bound Ab. OPG is useful for  
 assessing the ability of a candidate substance to bind to OPG. OPG NA is  
 useful for regulating the levels of OPG in an animal (human). The nucleic  
 acid promotes an increasing in tissue level of OPG. OPG is useful for  
 treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's  
 disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced  
 osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to  
 osteomyelitis, osteolytic metastasis, and periodontal bone loss. The  
 method further involves administering a substance chosen from bone  
 morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1  
 inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,  
 parathyroid hormone related protein and their analogues, E series of  
 prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is  
 useful for treating osteoporosis such as primary osteoporosis, endocrine  
 osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),  
 hereditary and congenital forms of osteoporosis (osteogenesis imperfecta  
 CC , homocystinuria, Menke's syndrome, and Riley-day syndrome) and  
 osteoporosis due to immobilisation of extremities, hypercalcaemia  
 resulting from solid tumours and haematologic malignancies (multiple  
 myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and  
 hypercalcaemia associated with hyperthyroidism and renal function  
 disorders, osteopaenia following surgery and osteonecrosis or bone cell  
 death. The present sequences is an OPG protein (or fragment).  
 XX  
 SQ Sequence 380 AA;

Query Match 94.6%; Score 2061; DB 8; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 2e-164;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 ETLPPKYLHYDPETGHQLCDKCAPGYLKQCHTVRRKTLVCPDHSYDTSWHTSDECV 81  
 Db 1 ETLPPKYLHYDPETGHQLCDKCAPGYLKQCHTVRRKTLVCPDHSYDTSWHTSDECV 60

Qy 82 YCSVCKELQSVKQECNRTNHRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERTNV 141  
 Db 61 YCSVCKELQSVKQECNRTNHRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERTNV 120

Qy 142 CKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATHDNCVSGNREATQKCGIDVTL 201  
 Db 121 CKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATHDNCVSGNREATQKCGIDVTL 180

Qy 202 CEEAFFRFAVPTKIIIPNWLVSVDLPSTGTVKNAESVERIKRRHSSQEQTFQLLKLWKHQ 261  
 Db 181 CEEAFFRFAVPTKIIIPNWLVSVDLPSTGTVKNAESVERIKRRHSSQEQTFQLLKLWKHQ 240

Qy 262 RDEMWVKIIQDIDLCESSVQRHLGSHNLTEQLLALMESLPCKISPEIERTRTKCS 321

Db 241 RDQEMVKKIQQDIDLCSSVQRHGHNSLTTEQLLALMESLPGRKKSIPESIERTRKTKS 300  
 QY 322 SEQLLKLLSLWRINKGDDTLKGLMYALKHLKTSHPFKTTHSLRKTRMLHSFTMYRLY 381  
 Db 301 SEQLLKLLSLWRINKGDDTLKGLMYALKHLKTSHPFKTTHSLRKTRMLHSFTMYRLY 360  
 QY 382 QKLFLEMIGNQVQSVKISCL 401  
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 11  
 ADM28861  
 ID ADM28861 standard; protein; 380 AA.  
 XX AC ADM28861;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Mouse osteoprotegerin cysteine-rich domains 1-4 plus C-terminus #2.  
 XX KW Mouse; OPG; bone resorption; excessive bone loss; osteoporosis;  
 KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;  
 KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;  
 KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;  
 KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;  
 KW Riley-day syndrome; immobilisation of extremity; tumour;  
 KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;  
 KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;  
 KW osteoprotegerin; transgenic.  
 XX OS Mus sp.  
 XX US2003027827-A1.  
 XX PD 06-NOV-2003.  
 XX PF 24-SEP-1999; 99US-00405032.  
 XX PR 22-DEC-1995; 95US-00577788.  
 PR 03-SEP-1996; 96US-00706945.  
 PR 20-DEC-1996; 96US-00717777.  
 PR 12-AUG-1998; 98US-00132985.  
 XX (BOYL/) BOYLE W J.  
 PA (LACE/) LACEY D L.  
 PA (CALZ/) CALZONE F J.  
 PA (CHAN/) CHANG M.  
 XX Boyle WJ, Lacey DL, Calzone FJ, Chang M;  
 WPI; 2004-041572/04.  
 XX Novel osteoprotegerin useful for treating conditions resulting in bone  
 PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone  
 PT loss caused by rheumatoid arthritis or osteomyelitis.  
 XX Example 6; Fig 12; 141pp; English.  
 XX The invention relates to a purified and isolated polypeptide having  
 CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or  
 CC having amino terminus at residue 22, and 1-216 amino acids are deleted  
 CC from carboxy terminus of human OPG polypeptide. Also included are an  
 CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression  
 CC vector comprising OPG NA, a host cell transformed or transfected with the  
 CC polypeptide comprising an amino acid sequence of the cell, producing OPG, a  
 CC acids comprising four cysteine-rich domains characteristic of the  
 CC cysteine rich domains of tumour necrosis factor receptor extracellular  
 CC regions (and an activity of increasing bone density), an antibody (Ab) or  
 CC its fragment which specifically binds to OPG, a composition comprising  
 CC OPG (in a carrier, adjuvant, stabiliser, and/or anti-oxidant)

CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.  
 CC Ab is useful for detecting the presence of OPG in a biological sample  
 CC which involves incubating the sample with Ab under conditions that allow  
 CC binding of Ab to OPG and detecting the bound Ab. OPG is useful for  
 CC assessing the ability of a candidate substance to bind to OPG. OPG NA is  
 CC useful for regulating the levels of OPG in an animal (human). The nucleic  
 CC acid promotes an increasing in tissue level of OPG. OPG is useful for  
 CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's  
 CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced  
 CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to  
 CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The  
 CC method further involves administering a substance chosen from bone  
 CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1  
 CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,  
 CC parathyroid hormone related protein and their analogues, E series of  
 CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is  
 CC useful for treating osteoporosis such as primary osteoporosis, endocrine  
 CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),  
 CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta  
 CC , homocystinuria, Menke's syndrome, and Riley-day syndrome) and  
 CC osteoporosis due to immobilisation of extremities, hypercalcaemia  
 CC resulting from solid tumours and haematologic malignancies (multiple  
 CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and  
 CC hypercalcaemia associated with hyperthyroidism and renal function  
 CC disorders, osteopaenia following surgery and osteonecrosis or bone cell  
 CC death. The present sequences is an OPG protein (or fragment).  
 XX SQ Sequence 380 AA;  
 Query Match 94.1%; Score 2050; DB 8; Length 380;  
 Best Local Similarity 99.2%; Pred. No. 1.7e-163;  
 Matches 377; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 22 ETLPPKYLHYDPTGHQLLCKAPGYLKQHTVRRKTLVCPDHSYDTSWHTSDECV 81  
 Db 1 ETLPPKYLHYDPTGHQLLCKAPGYLKQHTVRRKTLVCPDHSYDTSWHTSDECV 60  
 QY 82 YCSPVCKELQSVKQECNRTHNRVCECEGRYLBIEFCLKHRSPPGSGVQAGTPERTV 141  
 Db 61 YCSPVCKELQSVKQECNRTHNRVCECEGRYLBIEFCLKHRSPPGSGVQAGTPERTV 120  
 QY 142 CKKCPDGFSGTSSKAPCIKHTNCSTFGLLIQTGNATHDNYVCSGNREATQCGIDVTL 201  
 Db 121 CKKCPDGFSGTSSKAPCIKHTNCSTFGLLIQTGNATHDNYVCSGNREATQCGIDVTL 180  
 QY 202 CEAEFFRAVPTKIIIPNLSVLVDSLPGTKVNAESVERIKRHSSEQQTQLLKLWKHQN 261  
 Db 181 CEAEFFRAVPTKIIIPNLSVLVDSLPGTKVNAESVERIKRHSSEQQTQLLKLWKHQN 240  
 QY 262 RDQEMVKKIQQDIDLCSSVQRHGHNSLTTEQLLALMESLPGRKKSIPESIERTRKTKS 321  
 Db 241 RDQEMVKKIQQDIDLCSSVQRHGHNSLTTEQLLALMESLPGRKKSIPESIERTRKTKS 300  
 QY 322 SEQLLKLLSLWRINKGDDTLKGLMYALKHLKTSHPFKTTHSLRKTRMLHSFTMYRLY 381  
 Db 301 SEQLLKLLSLWRINKGDDTLKGLMYALKHLKTSHPFKTTHSLRKTRMLHSFTMYRLY 360  
 QY 382 QKLFLEMIGNQVQSVKISCL 401  
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 12  
 AAY05742  
 ID AAY05742 standard; protein; 401 AA.  
 XX AC AAY05742;  
 XX DT 19-JUL-1999 (first entry)  
 XX DE Tumour necrosis factor receptor TR1.  
 XX KW Tumour necrosis factor receptor; TR1; osteoprotegerin; agonist;

antagonist; screening; human; cancer; AIDS; Alzheimer's disease; inflammation; arthritis; septicemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; restenosis; brain injury; bone disease; atherosclerosis; therapy.

Homo sapiens.

EP911633-A1.

28-APR-1999.

02-OCT-1998; 98EP-00203332.

08-OCT-1997; 97US-0061334P.

(SMIK ) SMITHKLINE BEECHAM CORP.

McDonnell PC, Young PR, Zou J;

WPI; 1999-246560/21.

Identifying agonists and antagonists of tumor necrosis factor related receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of cancer, AIDS, Alzheimer's disease, bone disease etc.

Disclosure; Page 10-12; 23pp; English.

The present sequence represents tumour necrosis factor receptor (TNFR) TR1, also known as osteoprotegerin. The invention relates to TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and their ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in claimed methods of identifying agonists and antagonists, i.e. compounds that bind to the receptors or ligand, and which activate (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The agonists and antagonists are useful for treatment of chronic and acute inflammation, arthritis, septicemia, autoimmune disease e.g. inflammatory bowel disease, psoriasis, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 2; Length 401;  
Best Local Similarity 85.8%; Pred. No. 7.2e-151;  
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLDI-IEWTQETLPKYLHYDPETGQLLCKDCAPGYLKQHCTVRRK 59  
DB 1 MNKLLCCA-LVFLDISIKWTQETFPKYLHYDETSQQLLCKDCPPGYLKQHTAKWK 59

QY 60 TLVCPCPDHSTYDTSWHTSDSCVPCVKELQSVQECNRTNHRVCEEGRYLSEFCL 119  
DB 60 TVCAPCPDHYTDSWHTSDSCVPCVKELQSVQECNRTNHRVCEEGRYLSEFCL 119

QY 120 KHRSCPPGSGVQAGTPERTNCKCPDGFSGETSSKAPCIKHTNCSTFGLLLLQKNA 179  
DB 120 KHRSCPPGSGVQAGTPERTNCKCPDGFSGETSSKAPCRKHTNCSTFGLLLLQKNA 179

QY 180 THDNVCSGNREATKQGDIVLCEAFRAFPVTKIIPNWLVDLSLPGTKVNAESVER 239  
DB 180 THDNVCSGNSESTKQGDIVLCEAFRAFPVTKFTNWLVDLNLPGTKVNAESVER 239

QY 240 IKRHSQEQBTQLLKLWKHQNDQEMVKIIQDIDLCSSVQRHGLNSLTTQOLLALM 299  
DB 240 IKRHSQEQBTQLLKLWKHQNDQEMVKIIQDIDLCSSVQRHGLNSLTTQOLLALM 299

QY 300 ESLPGKKISPEIERTRKTKCSQELLKLLSLWRINKGQDQTLKGLMVALKHLKTSHPFK 359

DB 300 ESLPGKKVGAEDIENTKACKPSDQILKLLSLWRINKGQDQTLKGLMVALKHSKYHFK 359  
QY 360 TVTHSLRKTMRPLRHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
DB 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

RESULT 13  
AAW95030  
ID AAW95030 standard; protein; 401 AA.  
XX  
AC AAW95030;  
XX  
DT 13-MAY-1999 (first entry)  
XX  
DE Tumour necrosis factor receptor (TNF-R) related polypeptide TR1.  
XX  
KW Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL4; arthritis; inflammation; septicemia; autoimmune disease; transplant rejection; graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome; restenosis; bone disease; cancer; atherosclerosis; Alzheimer's disease.  
XX  
OS Unidentified.  
XX  
PN EP897114-A2.  
XX  
PD 17-FEB-1999.  
XX  
PF 04-JUN-1998; 98EP-00304424.  
XX  
PR 13-AUG-1997; 97US-0055513P.  
PR 26-AUG-1997; 97US-0056980P.  
PR 29-AUG-1997; 97US-0057550P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PI Brigham-Burke MR, Young PR;  
XX WPI; 1999-134308/12.  
XX  
PT Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (LR1, LR2, LR2 and LR4) - useful for treating stroke, Alzheimer's disease and AIDS.  
XX  
PS Disclosure; Page 11-12; 18pp; English.

XX The invention relates to identifying agonists or antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2 and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2 or TL4 with a candidate compound in the presence of TR1 or TR2; and (b) assessing the ability of the candidate compound to compete with TR1 or TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful for treating diseases caused by imbalance of TL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and Alzheimer's disease. The present sequence represents a TNF-R related polypeptide TR1

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 2; Length 401;  
Best Local Similarity 85.8%; Pred. No. 7.2e-151;  
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLDI-IEWTQETLPKYLHYDPETGQLLCKDCAPGYLKQHCTVRRK 59  
DB 1 MNKLLCCA-LVFLDISIKWTQETFPKYLHYDETSQQLLCKDCPPGYLKQHTAKWK 59

QY 60 TLVCPDHSYTDSTWHTSDCVYCSVPCKELQSVKQECNRTNHRVCECEGRYLETEFCL 119  
Db 60 TVCAPCPDHYTDSWHTSDCVYCSVPCKELQSVKQECNRTNHRVCECEGRYLETEFCL 119  
QY 120 KHRSCPPGSGVQVQAGTPPERNTVCKKCPDGFSSGETSSKAPCIKHNTNCSTFGLLLIQKNA 179  
Db 120 KHRSCPPGSGVQVQAGTPPERNTVCKKCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179  
QY 180 THDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKII PNWLSVLDLSLPGTKVNAESVER 239  
Db 180 THDNICSGNSESTQKCGIDVTLCCEAFPRFAVPTKFTPNWLSVLDNLPCTKVNAESVER 239  
QY 240 IKRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHNSLNTTEQLLALM 299  
Db 240 IKRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHNSLNTTEQLLALM 299  
QY 300 ESLPGKKISPEIERTRTKCKSEQLLKLKSLWRINKGQDQTLKGLMYALKHLKTSHPFK 359  
Db 300 ESLPGKKVGAEDIEKTIKACKPSDQILKLSLWRINKGQDQTLKGLMHALKHKSCTVHFPK 359  
QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 14

AAW83926  
ID AAW83926 standard; protein; 401 AA.

AC AAW83926;

XX 01-MAR-1999 (first entry)

XX Human FTHMA-070 protein.

XX FTHMA-070; human; neurological disorder; therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Protein /label= sig\_peptide

FT /label= Mat\_protein

XX WO9848051-A2.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-US007714.

XX 18-APR-1997; 97US-0044746P.

XX 10-OCT-1997; 97US-0062017P.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX McCarthy SA, Holtzman D;

XX WPI; 1999-024021/02.

XX N-PSDB; AAV69277.

XX New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.

XX Claim 8; Fig 1; 127pp; English.

XX This is the amino acid sequence of human FTHMA-070, a novel protein having homology to tumour necrosis factor receptor. The sequence was deduced from that of a cDNA clone (see AAV69277) isolated from a cardiac coronary artery smooth muscle cell library. FTHMA-070 nucleic acids and polypeptides of the invention are useful as modulating agents in regulating a variety of cellular processes. They can be used for

CC identifying compounds which bind to or modulate the activity of the polypeptides (claimed). They can also be used in screening assays, CC detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, CC monitoring clinical trials, and pharmacogenomics), and methods of CC treatment (e.g. therapeutic and prophylactic) e.g. for neurological disorders

XX Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 2; Length 401;

Best Local Similarity 85.8%; Pred. No. 7, 2e-151;

Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI-IEWTTOETLPPKYLHYDPTGHQLLCKDCAPGYLKHQCTVRRK 59

Db 1 MNKLLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKDCPPGYLKHQCTAKWK 59

QY 60 TLVCPDHSYTDSTWHTSDCVYCSVPCKELQSVKQECNRTNHRVCECEGRYLETEFCL 119

Db 60 TVCAPCPDHYTDSWHTSDCVYCSVPCKELQSVKQECNRTNHRVCECEGRYLETEFCL 119

QY 120 KHRSCPPGSGVQVQAGTPPERNTVCKKCPDGFSSGETSSKAPCIKHNTNCSTFGLLLIQKNA 179

Db 120 KHRSCPPGSGVQVQAGTPPERNTVCKKCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKNA 179

QY 180 THDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKII PNWLSVLDLSLPGTKVNAESVER 239

Db 180 THDNICSGNSESTQKCGIDVTLCCEAFPRFAVPTKFTPNWLSVLDNLPCTKVNAESVER 239

QY 240 IKRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHNSLNTTEQLLALM 299

Db 240 IKRRHSSQEQTFOLLKWKHQRNDQEMVKIIQDIDLCESSVQRHGHNSLNTTEQLLALM 299

QY 300 ESLPGKKISPEIERTRTKCKSEQLLKLKSLWRINKGQDQTLKGLMYALKHLKTSHPFK 359

Db 300 ESLPGKKVGAEDIEKTIKACKPSDQILKLSLWRINKGQDQTLKGLMHALKHKSCTVHFPK 359

QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 15

AAAB18715

ID AAB18715 standard; protein; 401 AA.

XX AAB18715;

XX 22-JAN-2001 (first entry)

XX A human tumour necrosis factor family receptor (TRI).

XX Human; tumour necrosis factor family receptor; TRI; tumour growth; cell proliferation; chlamydia infection; immunodeficiency; septic shock; T-cell mediated autoimmune disease; acquired immunodeficiency syndrome; AIDS; cerebral malaria; graft rejection; cytotoxicity; cachexia; KW apoptosis; inflammation; cancer; cardiovascular disease; angiogenesis; KW inflammatory disease; atherosclerosis; diabetes mellitus; allergy; KW neurological disorder; autoimmune disease; wound healing; bone formation; KW osteoporosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21 "signal peptide"

FT Protein /note= "mature protein"

XX WO200054651-A2.

XX 21-SEP-2000.

```
XX 15-MAR-2000; 2000WO-US0006592.
XX
XX 15-MAR-1999; 99US-0124489P.
XX 26-MAY-1999; 99US-0136248P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Greene JM, Fleischmann RD, Ni J;
XX WPI; 2000-618858/59.
XX DR N-PSDB; AAA75736.
XX
XX Novel tumor necrosis factor family receptor for diagnosing and treating
XX PT acquired immunodeficiency syndrome, cancer, cardiovascular diseases,
XX PT inflammatory diseases and autoimmune diseases.
XX
XX Claim 13; Fig 1A-B; 228pp; English.
XX
XX The present sequence represents a human tumour necrosis factor family
XX CC receptor (TRL) polypeptide. An agonist to the TRL receptor is useful for
XX CC inhibiting tumour growth, to stimulate human cellular proliferation, to
XX CC regulate immune response and antiviral response, to protect against the
XX CC effects of ionising radiations, to protect against chlamydia infections,
XX CC to regulate growth, and to treat immunodeficiencies such as in human
XX CC immunodeficiency virus (HIV). An antagonist to the TRL receptor is useful
XX CC for treating T-cell mediated autoimmune diseases, acquired
XX CC immunodeficiency syndrome (AIDS), septic shock, cerebral malaria, graft
XX CC rejection, cytotoxicity, cachexia, apoptosis, and inflammation. TRL
XX CC polynucleotides and polypeptides, and TRL agonists and antagonists are
XX CC useful for treating cancers, cardiovascular diseases, inflammatory
XX CC diseases, atherosclerosis, diabetes mellitus, neurological disorders,
XX CC autoimmune diseases, for promoting angiogenesis, for treating allergy,
XX CC for wound healing, for regulating bone formation and for treating
XX CC osteoporosis
XX
XX Sequence 401 AA;
XX
Query Match 87.2%; Score 1900; DB 3; Length 401;
Best Local Similarity 85.8%; Pred. No. 7.2e-151;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;
QY 1 MNKWLCCALLVLDI-IEWTTOETLPPKYLHYDPETHQOLLCDCAPGYLKHCTVRRK 59
Db 1 MNKLLCCA-LVFLDISIKWTTQETPPKYLHYDETSQOLLCDCPCPGTYLKQCTAKWK 59
QY 60 TLVCPGPDHSYDTSWHTSDECVCSVCKELQSVQECNRTNRYCECEGRYLEIFCL 119
Db 60 TVCAPCPDHYTDSWHTSDECLYCSPVCKELQVYQECNRTNRYCECKEGRYLEIFCL 119
QY 120 KHRSPGPGSGVVOAGTPERTNVCKKCPDGFPSGETSSKAPCIKHTNCSTFGLLLIQKNA 179
Db 120 KHRSPGPGSGVVOAGTPERTNVCKKCPDGFPSGETSSKAPCKHTNCSTFGLLLTQKNA 179
QY 180 THDNVCSGNREATKCGIDVTLCESAFRFAVPTKIIPNWLSVLDLPGTKVNAESVER 239
Db 180 THDNVCSGNSESTQKCGIDVTLCESAFRFAVPTKPTPNWLSVLDLPGTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKWQNRDQEMVKKIQQIDLCESVQRHLGHSNLTTEOLLALM 299
Db 240 IKRQHSSEQEFTQLLKWQNKQDQIVKKIQQIDLCENSQVRHIGHANLTFEQLRSLM 299
QY 300 ESLPGKKISPEIEIRTKTCKSSEQLLKLWLRIKNGDQDTLKLWYALKHKLKTSHPK 359
Db 300 ESLPGKVGAEIDIEKTIKACKPSQILKLLSWRIKNGDQDTLKLWYALKHKLKTSHPK 359
QY 360 TVTSHLRKTMRLHSFTMYRLYQKLFLEMIQNOVSQVKSICL 401
Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIQNOVSQVKSICL 401
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Search completed: March 8, 2005, 14:38:14  
Job time : 87.1064 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 21.9235 Seconds  
(without alignments)  
1365.399 Million cell updates/sec

Title: US-09-389-782A-2  
Perfect score: 2179  
Sequence: 1 MNKWLCCALLVLDIIETWT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2179	100.0	401	3 US-08-974-022-4	Sequence 4, Appli
2	2179	100.0	401	3 US-09-042-785A-13	Sequence 13, Appli
3	2179	100.0	401	3 US-08-795-445A-4	Sequence 4, Appli
4	2179	100.0	401	3 US-08-795-447A-4	Sequence 4, Appli
5	2179	100.0	401	3 US-08-974-186-4	Sequence 4, Appli
6	2179	100.0	401	3 US-08-795-446B-4	Sequence 4, Appli
7	2179	100.0	401	3 US-08-706-945D-126	Sequence 126, App
8	2179	100.0	401	4 US-08-577-788C-4	Sequence 4, Appli
9	2179	100.0	401	4 US-08-577-788C-54	Sequence 54, Appli
10	2079	95.4	401	3 US-08-374-022-2	Sequence 2, Appli
11	2079	95.4	401	3 US-08-795-445A-2	Sequence 2, Appli
12	2079	95.4	401	3 US-08-795-447A-2	Sequence 2, Appli
13	2079	95.4	401	3 US-08-974-186-2	Sequence 2, Appli
14	2079	95.4	401	3 US-08-795-446B-2	Sequence 2, Appli
15	2079	95.4	401	3 US-08-706-945D-124	Sequence 124, App
16	2079	95.4	401	4 US-08-577-788C-2	Sequence 2, Appli
17	2079	95.4	401	4 US-08-577-788C-55	Sequence 55, Appli
18	1955	89.7	364	3 US-08-706-945D-141	Sequence 141, App
19	1900	87.2	401	3 US-09-153-927-1	Sequence 1, Appli
20	1900	87.2	401	3 US-09-072-993C-1	Sequence 1, Appli
21	1892	86.8	401	3 US-08-974-022-6	Sequence 12, Appli
22	1892	86.8	401	3 US-09-042-785A-12	Sequence 12, Appli
23	1892	86.8	401	3 US-08-795-445A-6	Sequence 6, Appli
24	1892	86.8	401	3 US-08-795-447A-6	Sequence 6, Appli
25	1892	86.8	401	3 US-08-974-186-6	Sequence 6, Appli
26	1892	86.8	401	3 US-08-795-446B-6	Sequence 6, Appli
27	1892	86.8	401	3 US-08-706-945D-128	Sequence 128, App

28	1892	86.8	401	4 US-08-577-788C-6	Sequence 6, Appli
29	1892	86.8	401	4 US-08-577-788C-56	Sequence 56, Appli
30	1892	86.8	401	4 US-09-064-832-2	Sequence 2, Appli
31	1727	79.3	364	3 US-08-706-945D-142	Sequence 142, App
32	1427	65.5	293	4 US-09-896-096A-18	Sequence 18, Appli
33	1128	51.8	208	4 US-08-577-788C-50	Sequence 50, Appli
34	946	43.4	174	3 US-08-706-945D-136	Sequence 136, App
35	838	38.5	161	4 US-09-632-277A-3	Sequence 3, Appli
36	768	35.2	147	3 US-09-527-236A-20	Sequence 20, Appli
37	768	35.2	147	4 US-09-756-854-20	Sequence 20, Appli
38	764	35.1	146	4 US-09-523-323-58	Sequence 58, Appli
39	731	33.5	139	3 US-08-706-945D-130	Sequence 130, App
40	424.5	19.5	271	4 US-09-936-019-1	Sequence 1, Appli
41	424.5	19.5	300	2 US-08-794-796-2	Sequence 2, Appli
42	424.5	19.5	300	4 US-09-632-277A-2	Sequence 2, Appli
43	424.5	19.5	300	4 US-09-523-323-52	Sequence 52, Appli
44	424.5	19.5	300	4 US-09-896-096A-1	Sequence 1, Appli
45	424.5	19.5	300	4 US-09-936-019-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-974-022-4  
; Sequence 4, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Denavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,022  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-974-022-4

Query Match 100.0%; Score 2179; DB 3; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNKLCCALLVLDIIETWTQTLPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKT	60
DB	1	MNKLCCALLVLDIIETWTQTLPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKT	60
QY	61	LCVPCPDHSYTDSTWHTSDCVYCSVCKELQSQECNTRNRCBEGRYLEIFCLK	120

Db 61 LCVPDPHSYDTSWHTSDECVYCSVPCKELQSVKQECNRTNHRVCECEGRYLEIEFCLK 120  
Qy 121 HRSPPGSGVQAGTPERNTVCKKCPDGFPSGETSKAPCIKHTNCSTFGLLIQKGNAT 180  
Db 121 HRSPPGSGVQAGTPERNTVCKKCPDGFPSGETSKAPCIKHTNCSTFGLLIQKGNAT 180  
Qy 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240  
Db 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240  
Qy 241 KRRHSSQBOTFOLLKWKHONRDQEMVKIIQDIDLCESSVQRHGHSLNLTTEQLLALME 300  
Db 241 KRRHSSQBOTFOLLKWKHONRDQEMVKIIQDIDLCESSVQRHGHSLNLTTEQLLALME 300  
Qy 301 SLPGKKISPEEIERTRTKCKSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360  
Db 301 SLPGKKISPEEIERTRTKCKSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360  
Qy 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

## RESULT 2

US-09-042-785A-13  
; Sequence 13, Application US/09042785A  
; Patent No. 6194151  
; GENERAL INFORMATION:  
; APPLICANT: Busfield, Samantha J  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; City: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,785A  
; FILING DATE: 17-MAR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/938,896  
; FILING DATE: 26-SEP-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MEI-001CP  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-09-042-785A-13

Query Match 100.0%; Score 2179; DB 3; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKKCAPGTLYLKQHCCTVRKKT 60  
|||||

Db 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKKCAPGTLYLKQHCCTVRKKT 60  
Qy 61 LCVPDPHSYDTSWHTSDECVYCSVPCKELQSVKQECNRTNHRVCECEGRYLEIEFCLK 120  
Db 61 LCVPDPHSYDTSWHTSDECVYCSVPCKELQSVKQECNRTNHRVCECEGRYLEIEFCLK 120  
Qy 121 HRSPPGSGVQAGTPERNTVCKKCPDGFPSGETSKAPCIKHTNCSTFGLLIQKGNAT 180  
Db 121 HRSPPGSGVQAGTPERNTVCKKCPDGFPSGETSKAPCIKHTNCSTFGLLIQKGNAT 180  
Qy 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240  
Db 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKII PNWLSVLDLPGTKVNAESVERI 240  
Qy 241 KRRHSSQBOTFOLLKWKHONRDQEMVKIIQDIDLCESSVQRHGHSLNLTTEQLLALME 300  
Db 241 KRRHSSQBOTFOLLKWKHONRDQEMVKIIQDIDLCESSVQRHGHSLNLTTEQLLALME 300  
Qy 301 SLPGKKISPEEIERTRTKCKSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360  
Db 301 SLPGKKISPEEIERTRTKCKSEQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPFKT 360  
Qy 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

## RESULT 3

US-08-795-445A-4  
; Sequence 4, Application US/08795445A  
; Patent No. 6284485  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; City: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,445A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-445A-4

Query Match 100.0%; Score 2179; DB 3; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKKCAPGTLYLKQHCCTVRKKT 60  
|||||

Db 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQCHTVRRKT 60  
QY 61 LCVPDPHSDYTDWHTSDECVYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
Db 61 LCVPDPHSDYTDWHTSDECVYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
QY 121 HRSPPGSGVQAGTVPRTNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180  
Db 121 HRSPPGSGVQAGTVPRTNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180  
QY 181 HDNVCSGNREATKCGIDVTLCBEAFRFAVPTKIIIPNMLSVLVDSPGTVKNAESVERI 240  
Db 181 HDNVCSGNREATKCGIDVTLCBEAFRFAVPTKIIIPNMLSVLVDSPGTVKNAESVERI 240  
QY 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDIDLCESVQRHLGHSNLTTEQLLALME 300  
Db 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDIDLCESVQRHLGHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEIERTRTKTCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360  
Db 301 SLPGKKISPEIERTRTKTCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 4

US-08-795-447A-4  
; Sequence 4, Application US/08795447A  
; Patent No. 6284728  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: One Amgen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91362-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,447A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378D2  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-447A-4

Query Match 100.0%; Score 2179; DB 3; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQCHTVRRKT 60  
Db 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQCHTVRRKT 60

QY 61 LCVPDPHSDYTDWHTSDECVYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
Db 61 LCVPDPHSDYTDWHTSDECVYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
QY 121 HRSPPGSGVQAGTVPRTNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180  
Db 121 HRSPPGSGVQAGTVPRTNVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQGNAT 180  
QY 181 HDNVCSGNREATKCGIDVTLCBEAFRFAVPTKIIIPNMLSVLVDSPGTVKNAESVERI 240  
Db 181 HDNVCSGNREATKCGIDVTLCBEAFRFAVPTKIIIPNMLSVLVDSPGTVKNAESVERI 240  
QY 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDIDLCESVQRHLGHSNLTTEQLLALME 300  
Db 241 KRRHSSQEQTFQLLWKHQNDRQEMVKIIQIDIDLCESVQRHLGHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEIERTRTKTCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360  
Db 301 SLPGKKISPEIERTRTKTCKSSBQLLKLWLRIKNGDQDTLKGMLYALKHLKTSHPPKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 5

US-08-974-186-4  
; Sequence 4, Application US/08974186  
; Patent No. 6284740  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPTROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,186  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/577,788  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-974-186-4

Query Match 100.0%; Score 2179; DB 3; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQCHTVRRKT 60  
Db 1 MNKWLCCALLVLLDIETWTTQETLPKYLHYDPETHGQLLCKDCAPGYLKQCHTVRRKT 60

Db 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60  
QY 61 LCVPCPDHSYTDSDWHTSDCVYCSVKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120  
Db 61 LCVPCPDHSYTDSDWHTSDCVYCSVKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120  
QY 121 HRSPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
Db 121 HRSPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
QY 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNWLVDLSLPGTKVNAESVERI 240  
Db 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNWLVDLSLPGTKVNAESVERI 240  
QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLAME 300  
Db 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLAME 300  
QY 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLWRINKGDQDTLKGMLVALKHLKTSHPFKT 360  
Db 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLWRINKGDQDTLKGMLVALKHLKTSHPFKT 360  
QY 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
Db 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 6

US-08-795-446B-4  
; Sequence 4, Application US/08795446B  
; Patent No. 6288032  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; PRIORITY DATE:  
; PRIOR APPLICATION DATA:  
; FILING DATE: 08/577,788  
; APPLICATION NUMBER: 08/577,788  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-446B-4

Query Match 100.0%; Score 2179; DB 3; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60

Db 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60  
QY 61 LCVPCPDHSYTDSDWHTSDCVYCSVKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120  
Db 61 LCVPCPDHSYTDSDWHTSDCVYCSVKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120  
QY 121 HRSPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
Db 121 HRSPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
QY 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNWLVDLSLPGTKVNAESVERI 240  
Db 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNWLVDLSLPGTKVNAESVERI 240  
QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLAME 300  
Db 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLAME 300  
QY 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLWRINKGDQDTLKGMLVALKHLKTSHPFKT 360  
Db 301 SLPGKKISPEEIERTRKTKSSEQLLKLSLWRINKGDQDTLKGMLVALKHLKTSHPFKT 360  
QY 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
Db 361 VTHSLRKTMRFHLSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 7

US-08-706-945D-126  
; Sequence 126, Application US/08706945D  
; Patent No. 6369027  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Lacey, David  
; APPLICANT: Calzone, Frank  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378CIP  
; CURRENT APPLICATION NUMBER: US/08/706,945D  
; CURRENT FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/577,788  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 126  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-706-945D-126

Query Match 100.0%; Score 2179; DB 3; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60  
Db 1 MNKWLCCALLVLLDIIIEWTTQETLPPKYLHYDPETGHQLLCKCAPGTYLKQHCIVRRKT 60  
QY 61 LCVPCPDHSYTDSDWHTSDCVYCSVKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120  
Db 61 LCVPCPDHSYTDSDWHTSDCVYCSVKELQSVKQECNTHNRVCECEBGRYLEIEFCLK 120  
QY 121 HRSPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
Db 121 HRSPPGSGVVOAGTPERNTVCKCPDGFSGSETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
QY 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNWLVDLSLPGTKVNAESVERI 240  
Db 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNWLVDLSLPGTKVNAESVERI 240  
QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKKIIQDIDLCESSVQRHGHNSLTTEQLLAME 300

Db 241 KRRHSSQEQTFQLLKLVKWHQNRDQEMVKKIIQIDIDLCESSVQRHGLHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEIERTRTKTCKSSBQLLKLKLSLWIRKNGDQDTLKLGLMYALKHLKLTSHPPKT 360  
Db 301 SLPGKKISPEIERTRTKTCKSSBQLLKLKLSLWIRKNGDQDTLKLGLMYALKHLKLTSHPPKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 8

US-08-577-788C-4  
; Sequence 4, Application US/08577788C  
; Patent No. 6613544  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Lacey, David  
; APPLICANT: Calzone, Frank  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378 Rev  
; CURRENT APPLICATION NUMBER: US/08/577,788C  
; CURRENT FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-577-788C-4

Query Match 100.0%; Score 2179; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDPTGHQLLCKDCAPGYLKQHTVRRKT 60  
Db 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDPTGHQLLCKDCAPGYLKQHTVRRKT 60  
QY 61 LCVPCPDHSTYDSWHTSDCEVCYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
Db 61 LCVPCPDHSTYDSWHTSDCEVCYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
QY 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFPSGETSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
Db 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFPSGETSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
QY 181 HDNVCSGNREATQKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSLPGTKVNAESVERI 240  
Db 181 HDNVCSGNREATQKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSLPGTKVNAESVERI 240  
QY 241 KRRHSSQEQTFQLLKLVKWHQNRDQEMVKKIIQIDIDLCESSVQRHGLHSNLTTEQLLALME 300  
Db 241 KRRHSSQEQTFQLLKLVKWHQNRDQEMVKKIIQIDIDLCESSVQRHGLHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEIERTRTKTCKSSBQLLKLKLSLWIRKNGDQDTLKLGLMYALKHLKLTSHPPKT 360  
Db 301 SLPGKKISPEIERTRTKTCKSSBQLLKLKLSLWIRKNGDQDTLKLGLMYALKHLKLTSHPPKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 9

US-08-577-788C-54  
; Sequence 54, Application US/08577788C  
; Patent No. 6613544  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Lacey, David  
; APPLICANT: Calzone, Frank  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378 Rev  
; CURRENT APPLICATION NUMBER: US/08/577,788C  
; CURRENT FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-577-788C-54

; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378 Rev  
; CURRENT APPLICATION NUMBER: US/08/577,788C  
; CURRENT FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-577-788C-54

Query Match 100.0%; Score 2179; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.3e-195;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDPTGHQLLCKDCAPGYLKQHTVRRKT 60  
Db 1 MNKWLCCALLVLDIIEWTTQETLPPKYLHYDPTGHQLLCKDCAPGYLKQHTVRRKT 60  
QY 61 LCVPCPDHSTYDSWHTSDCEVCYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
Db 61 LCVPCPDHSTYDSWHTSDCEVCYSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCLK 120  
QY 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFPSGETSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
Db 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFPSGETSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
QY 181 HDNVCSGNREATQKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSLPGTKVNAESVERI 240  
Db 181 HDNVCSGNREATQKCGIDVTLCBAAFRAVPTKIIIPNLSVLVDSLPGTKVNAESVERI 240  
QY 241 KRRHSSQEQTFQLLKLVKWHQNRDQEMVKKIIQIDIDLCESSVQRHGLHSNLTTEQLLALME 300  
Db 241 KRRHSSQEQTFQLLKLVKWHQNRDQEMVKKIIQIDIDLCESSVQRHGLHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEIERTRTKTCKSSBQLLKLKLSLWIRKNGDQDTLKLGLMYALKHLKLTSHPPKT 360  
Db 301 SLPGKKISPEIERTRTKTCKSSBQLLKLKLSLWIRKNGDQDTLKLGLMYALKHLKLTSHPPKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 10

US-08-974-022-2  
; Sequence 2, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,022  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION:

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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-2

Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 3e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRKT 60
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Db 61 LCVPCHSHSYTDSWHTSDECVYSPVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFFSGTSSKAPCIKHTNGSTFGLLIIOKGNAT 180
Db 121 HRSCPPGLVQAGTPERNTVCKKCPDGFFSGTSSKAPCRKHTNCSSGLGLLIIOKGNAT 180
QY 181 HDNVCSGNREATQCGIDVTLCCEAFPRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
Db 181 HDNVCSGNREATQCGIDVTLCCEAFPRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
QY 241 KRRHSSQEQTFQLLWKQHNQDQEMVKKIIQDIDLCSSVQRHGHNSLTTEQLLALME 300
Db 241 KRRHSSQEQTFQLLWKQHNQDQEMVKKIIQDIDLCSSVQRHGHNSLTTEQLLALME 300
QY 301 SLPGKKISPEIERTRKTKSSQOLLKLSLWRKNGDQDTLKGMLYALKHLSHPFKT 360
Db 301 SLPGKKISPEIERTRKTKSSQOLLKLSLWRKNGDQDTLKGMLYALKHLSHPFKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 11
US-08-795-445A-2
; Sequence 2, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:

;
;
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-445A-2

Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 3e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRKT 60
Db 1 MNKWLCCALLVLDIIIEWTTQETLPPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRKT 60
QY 61 LCVPCHSHSYTDSWHTSDECVYSPVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
Db 61 LCVPCHSHSYTDSWHTSDECVYSPVCKELQSVKQECNTHNRVCECEGRYLEIEFCLK 120
QY 121 HRSCPPGSGVQAGTPERNTVCKKCPDGFFSGTSSKAPCIKHTNGSTFGLLIIOKGNAT 180
Db 121 HRSCPPGLVQAGTPERNTVCKKCPDGFFSGTSSKAPCRKHTNCSSGLGLLIIOKGNAT 180
QY 181 HDNVCSGNREATQCGIDVTLCCEAFPRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
Db 181 HDNVCSGNREATQCGIDVTLCCEAFPRFAVPTKIIIPNWLVSVDLPSTGKVAESVERI 240
QY 241 KRRHSSQEQTFQLLWKQHNQDQEMVKKIIQDIDLCSSVQRHGHNSLTTEQLLALME 300
Db 241 KRRHSSQEQTFQLLWKQHNQDQEMVKKIIQDIDLCSSVQRHGHNSLTTEQLLALME 300
QY 301 SLPGKKISPEIERTRKTKSSQOLLKLSLWRKNGDQDTLKGMLYALKHLSHPFKT 360
Db 301 SLPGKKISPEIERTRKTKSSQOLLKLSLWRKNGDQDTLKGMLYALKHLSHPFKT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 12
US-08-795-447A-2
; Sequence 2, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
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;; FILING DATE: 514  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winter, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-378D2  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 401 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-795-447A-2

Query Match 95.4%; Score 2079; DB 3; Length 401;  
Best Local Similarity 94.5%; Pred. No. 3e-186;  
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60  
DB 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60  
QY 61 LCVPCPDHSDYSDSWHTSDECVYSPVCKELQSVKQECNTRNVRVCECEGRYLEIEFCLK 120  
DB 61 LCVPCPDYSDSWHTSDECVYSPVCKELQSVKQECNTRNVRVCECEGRYLEIEFCLK 120  
QY 121 HRSPGPGVGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
DB 121 HRSPGPGVGVQAGTPERNTVCKCPDGFSGTSSKAPCRKHTNCSLGLLLIQKGNAT 180  
QY 181 HDNVCNREATQCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240  
DB 181 HDNVCNREATQCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240  
QY 241 KRRHSSQEQTFQLLKLWKHQNDRDQEMVKIIQIDIDLCESVQRHGLHSNLTTEQLLALME 300  
DB 241 KRRHSSQEQTFQLLKLWKHQNDRDQEMVKIIQIDIDLCESVQRHGLHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEIERTRKTKCSSQOLLKLSLWRIKNGDQDTLGLMYALKHLKTSHPPKT 360  
DB 301 SLPGKKISPEIERTRKTKCSSQOLLKLSLWRIKNGDQDTLGLMYALKHLKAYHPPKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
DB 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 13

US-08-974-186-2  
; Sequence 2, Application US/08974186  
; Patent No. 6284740  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,186  
; FILING DATE:  
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:  
;; FILING DATE: 08/577,788  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winter, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-378  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 401 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-974-186-2

Query Match 95.4%; Score 2079; DB 3; Length 401;  
Best Local Similarity 94.5%; Pred. No. 3e-186;  
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60  
DB 1 MNKWLCCALLVLDIIIEWTTQETLPKYLHYDDETHGQLLCKDCAPGTYLKQHCTVRRKT 60  
QY 61 LCVPCPDHSDYSDSWHTSDECVYSPVCKELQSVKQECNTRNVRVCECEGRYLEIEFCLK 120  
DB 61 LCVPCPDYSDSWHTSDECVYSPVCKELQSVKQECNTRNVRVCECEGRYLEIEFCLK 120  
QY 121 HRSPGPGVGVQAGTPERNTVCKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
DB 121 HRSPGPGVGVQAGTPERNTVCKCPDGFSGTSSKAPCRKHTNCSLGLLLIQKGNAT 180  
QY 181 HDNVCNREATQCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240  
DB 181 HDNVCNREATQCGIDVTLCEAEPFAVPPTKIIPNWLVLVDSIPGTVKNAESVERI 240  
QY 241 KRRHSSQEQTFQLLKLWKHQNDRDQEMVKIIQIDIDLCESVQRHGLHSNLTTEQLLALME 300  
DB 241 KRRHSSQEQTFQLLKLWKHQNDRDQEMVKIIQIDIDLCESVQRHGLHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEIERTRKTKCSSQOLLKLSLWRIKNGDQDTLGLMYALKHLKTSHPPKT 360  
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QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
DB 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401

## RESULT 14

US-08-795-446B-2  
; Sequence 2, Application US/08795446B  
; Patent No. 6288032  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,446B  
; FILING DATE:

; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/577,788  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winter, Robert B.  
 ; REFERENCE/DOCKET NUMBER: A-378  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 401 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-795-446B-2

Query Match 95.4%; Score 2079; DB 3; Length 401;  
 Best Local Similarity 94.5%; Pred. No. 3e-186;  
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 MNKWLCCALLVLDDIIIEWTTQETLPPKYLHYDPETHGQLLCKDCAPGTYLKQHCCTVRRKT 60  
 Db 1 MNKWLCCALLVFLDIIIEWTTQETLPPKYLHYDPETHGQLLCKDCAPGTYLKQHCCTVRRKT 60  
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 Db 121 HRSCPPGLGVLOAGTPERNTVCKCPDGFSSGSETSSKAPCRKHTNCSSLGILLIQQGNAT 180  
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIIPNWLSDLVDSLPQTKVNAESVERI 240  
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 Db 301 SLPCKKISPEIEIRTRKTCSSBQLLKLWLRIKNGDQDTLKGIMYALKHLKTSHPFKT 360  
 QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
 Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

## RESULT 15

US-08-706-945D-124  
 ; Sequence 124, Application US/08706945D  
 ; Patent No. 6369027  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyle, William  
 ; APPLICANT: Lacey, David  
 ; APPLICANT: Calzone, Frank  
 ; APPLICANT: Chang, Ming-Shi  
 ; TITLE OF INVENTION: Osteoprotegerin  
 ; FILE REFERENCE: A-378CIP  
 ; CURRENT APPLICATION NUMBER: US/08/706,945D  
 ; PRIOR FILING DATE: 1996-09-03  
 ; PRIOR APPLICATION NUMBER: 08/577,788  
 ; PRIOR FILING DATE: 1995-12-22  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 124  
 ; LENGTH: 401  
 ; TYPE: PRT  
 ; ORGANISM: Rattus rattus  
 ; US-08-706-945D-124

Query Match 95.4%; Score 2079; DB 3; Length 401;  
 Best Local Similarity 94.5%; Pred. No. 3e-186;

Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
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 Db 1 MNKWLCCALLVFLDIIIEWTTQETLPPKYLHYDPETHGQLLCKDCAPGTYLKQHCCTVRRKT 60  
 QY 61 LCVPCPDHSYTDSSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEBGRYLEIEFCLK 120  
 Db 61 LCVPCPDYSYTDSSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEBGRYLEIEFCLK 120  
 QY 121 HRSCPPGSGVVOAGTPERNTVCKCPDGFSSGSETSSKAPCIKHTNCSTFGLLLIQKGNAT 180  
 Db 121 HRSCPPGLGVLOAGTPERNTVCKCPDGFSSGSETSSKAPCRKHTNCSSLGILLIQQGNAT 180  
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIIPNWLSDLVDSLPQTKVNAESVERI 240  
 Db 181 HDNVCSGNREATQNGCIDVTLCCEAFPRFAVPTKIIIPNWLSDLVDSLPQTKVNAESVERI 240  
 QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGHANLTTEQLRLME 300  
 Db 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHGHANLTTEQLRLME 300  
 QY 301 SLPCKKISPEIEIRTRKTCSSBQLLKLWLRIKNGDQDTLKGIMYALKHLKTSHPFKT 360  
 Db 301 SLPCKKISPEIEIRTRKTCSSBQLLKLWLRIKNGDQDTLKGIMYALKHLKTSHPFKT 360  
 QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
 Db 361 VTHSLRKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Search completed: March 8, 2005, 14:48:09  
 Job time : 31.9235 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 60.5885 Seconds  
(without alignments)  
2177.757 Million cell updates/sec

Title: US-09-389-782a-2

Perfect score: 2179  
Sequence: 1 MNKWLCCALLVLDIIETWT.....QKLFLFMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	2061	94.6	380	10	US-09-405-032-138
5	1900	87.2	401	13	US-10-066-209-1
6	1900	87.2	401	13	US-10-105-934-2
7	1900	87.2	401	13	US-10-164-592-2
8	1900	87.2	401	14	US-10-044-674-3
9	1900	87.2	401	14	US-10-322-673-5
10	1900	87.2	401	14	US-10-139-785-5
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13	1895	87.0	401	14	US-10-183-091-1
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15	1895	87.0	401	14	US-10-232-858-5	Sequence 5, Appli
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18	1895	87.0	401	16	US-10-785-114-5	Sequence 5, Appli
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20	1895	87.0	401	17	US-10-929-748-5	Sequence 5, Appli
21	1892	86.8	401	10	US-09-405-032-125	Sequence 125, App
22	1892	86.8	401	14	US-10-151-071-8	Sequence 8, Appli
23	1892	86.8	401	16	US-10-467-243-2	Sequence 2, Appli
24	1892	86.8	401	17	US-10-129-595-3	Sequence 3, Appli
25	1892	86.6	400	14	US-10-142-658-2	Sequence 2, Appli
26	1895	86.5	401	9	US-09-062-113-62	Sequence 62, Appli
27	1895	86.5	401	9	US-09-062-113-63	Sequence 63, Appli
28	1895	86.5	401	9	US-09-062-113-64	Sequence 64, Appli
29	1895	86.5	401	9	US-09-062-113-65	Sequence 65, Appli
30	1895	86.5	401	9	US-09-062-113-66	Sequence 66, Appli
31	1895	86.5	401	14	US-10-232-858-62	Sequence 62, Appli
32	1895	86.5	401	14	US-10-232-858-63	Sequence 63, Appli
33	1895	86.5	401	14	US-10-232-858-64	Sequence 64, Appli
34	1895	86.5	401	14	US-10-232-858-65	Sequence 65, Appli
35	1895	86.5	401	14	US-10-232-858-66	Sequence 66, Appli
36	1895	86.5	401	16	US-10-785-109-62	Sequence 62, Appli
37	1895	86.5	401	16	US-10-785-109-63	Sequence 63, Appli
38	1895	86.5	401	16	US-10-785-109-64	Sequence 64, Appli
39	1895	86.5	401	16	US-10-785-109-65	Sequence 65, Appli
40	1895	86.5	401	16	US-10-785-109-66	Sequence 66, Appli
41	1895	86.5	401	16	US-10-785-114-62	Sequence 62, Appli
42	1895	86.5	401	16	US-10-785-114-63	Sequence 63, Appli
43	1895	86.5	401	16	US-10-785-114-64	Sequence 64, Appli
44	1895	86.5	401	16	US-10-785-114-65	Sequence 65, Appli
45	1895	86.5	401	16	US-10-785-114-66	Sequence 66, Appli

#### ALIGNMENTS

RESULT 1  
US-09-389-782-2  
; Sequence 2, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-2

Query Match 100.0%; Score 2179; DB 10; Length 401;  
Best Local Similarity 100.0%; Pred. No. 3.3e-171;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNKLCCALLVLDIIETWTQETLPPKYLHYDPTGHLLCDKCAPGTYLKQHCTVRRKT	60
DB	1	MNKLCCALLVLDIIETWTQETLPPKYLHYDPTGHLLCDKCAPGTYLKQHCTVRRKT	60
QY	61	LCVPCPDHSVTDSWHTSDSCVYCSVKELQSVKQCNRTHNRVCEBGRYLEIFCLK	120
DB	61	LCVPCPDHSVTDSWHTSDSCVYCSVKELQSVKQCNRTHNRVCEBGRYLEIFCLK	120
QY	121	HRSCPPGSGVQAGTPTNRTVCKCPDGFSGTSSKAPCIKHTNCGSTFGLLIQKGNAT	180
DB	121	HRSCPPGSGVQAGTPTNRTVCKCPDGFSGTSSKAPCIKHTNCGSTFGLLIQKGNAT	180

QY 181 HDNVCNREATQKCGIDVTLCEAFAFFFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240  
DB 181 HDNVCNREATQKCGIDVTLCEAFAFFFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240  
QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360  
DB 301 SLPGKKISPEERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
DB 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
RESULT 2  
US-09-405-032-123  
; Sequence 123, Application US/09405032  
; Publication No. US20030207827A1  
; GENERAL INFORMATION:  
; APPLICANT: Amgen Inc.  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 168  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/405,032  
; FILING DATE: 24-Sep-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wintek, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378-CIP2  
; INFORMATION FOR SEQ ID NO: 123:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-09-405-032-123  
Query Match 100.0%; Score 2179; DB 10; Length 401;  
Best Local Similarity 100.0%; Pred. No. 3.3e-171;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60  
DB 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60  
QY 61 LCVPCPDHSYTDSWHTSDSCVYCSVPVKELQSVQECNRTNHRVCECEBGRYLEIEFCLK 120  
DB 61 LCVPCPDHSYTDSWHTSDSCVYCSVPVKELQSVQECNRTNHRVCECEBGRYLEIEFCLK 120  
QY 121 HRSCPPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
DB 121 HRSCPPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
QY 181 HDNVCNREATQKCGIDVTLCEAFAFFFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240  
DB 181 HDNVCNREATQKCGIDVTLCEAFAFFFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240

QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
QY 301 SLPGKKISPEERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360  
DB 301 SLPGKKISPEERTRKTKCSSEQLLKLSLWRINKGDDOTLKGLMYALKHLKTSHPFKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
DB 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
RESULT 3  
US-09-405-032-121  
; Sequence 121, Application US/09405032  
; Publication No. US20030207827A1  
; GENERAL INFORMATION:  
; APPLICANT: Amgen Inc.  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 168  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/405,032  
; FILING DATE: 24-Sep-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wintek, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378-CIP2  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 121:  
US-09-405-032-121  
Query Match 95.4%; Score 2079; DB 10; Length 401;  
Best Local Similarity 94.5%; Pred. No. 5.9e-163;  
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60  
DB 1 MNKWLCCALLVLDIIETWTQETLPPKYLHYDPETGHQLLCKDCAPGYLKHQCTVRRKT 60  
QY 61 LCVPCPDHSYTDSWHTSDSCVYCSVPVKELQSVQECNRTNHRVCECEBGRYLEIEFCLK 120  
DB 61 LCVPCPDHSYTDSWHTSDSCVYCSVPVKELQSVQECNRTNHRVCECEBGRYLEIEFCLK 120  
QY 121 HRSCPPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
DB 121 HRSCPPGSGVGVQAGTPERTNVCCKPDGFFSGETSSKAPCIKHTNCSTFGLLLIQGNAT 180  
QY 181 HDNVCNREATQKCGIDVTLCEAFAFFFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240  
DB 181 HDNVCNREATQKCGIDVTLCEAFAFFFAVPTKIIIPNWLVLVDSLPGTKVNAESVERI 240  
QY 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300  
DB 241 KRRHSSQEQTFOLLKWLKHQNRDQEMVKIIQDIDLCESSVQRHLGHSNLTTEQLLALME 300

QY 301 SLPGKISPEIRTRKTKSSBOLLKLLSLWRIKNGDQDTLGLMYALKHKTSHPEPKT 360  
Db 301 SLPGKISPEIRTRKTKSPBOLLKLLSLWRIKNGDQDTLGLMYALKHKTSHPEPKT 360  
QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
Db 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

## RESULT 4

US-09-405-032-138  
; Sequence 138, Application US/09405032  
; Publication No. US20030207827A1  
; GENERAL INFORMATION:  
; APPLICANT: Amgen Inc.  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 168  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/405,032  
; FILING DATE: 24-Sep-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378-CIP2  
; INFORMATION FOR SEQ ID NO: 138:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 380 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 138:  
US-09-405-032-138

Query Match 94.6%; Score 2061; DB 10; Length 380;  
Best Local Similarity 100.0%; Pred. No. 1.7e-161;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ETLPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKTLVCPDHSYTDSDWHTSDECY 81  
Db 1 ETLPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRKTLVCPDHSYTDSDWHTSDECY 60  
QY 82 YCSFVKELQSVQECNRTHNRVCEBEGRYLIEFCLKRSPPGSGVVGAGTPEINTV 141  
Db 61 YCSFVKELQSVQECNRTHNRVCEBEGRYLIEFCLKRSPPGSGVVGAGTPEINTV 120  
QY 142 CKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATHDNCVSGNRREATKCGIDVTL 201  
Db 121 CKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATHDNCVSGNRREATKCGIDVTL 180  
QY 202 CEEAFFRFAVPTKIIPNLSVLVDSLPGTKNVASEVERIKRRHSSQEQTFQLLKWKHQN 261  
Db 181 CEEAFFRFAVPTKIIPNLSVLVDSLPGTKNVASEVERIKRRHSSQEQTFQLLKWKHQN 240  
QY 262 RDEWVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALMESLPCKKISPEIERTRKTKS 321  
Db 241 RDEWVKKIIQDIDLCESSVQRHLGHSNLTTEQLLALMESLPCKKISPEIERTRKTKS 300  
QY 322 SEQLLKLSLWRIKNGDQDTLGLMYALKHKTSHPEPKTVTHSLRKTMRFLHSFTMYRLY 381  
Db 301 SEQLLKLSLWRIKNGDQDTLGLMYALKHKTSHPEPKTVTHSLRKTMRFLHSFTMYRLY 360

QY 382 OKLFLEMIGNQVQSVKISCL 401  
Db 361 OKLFLEMIGNQVQSVKISCL 380

## RESULT 5

US-10-066-209-1  
; Sequence 1, Application US/10066209  
; Publication No. US20020115110A1  
; GENERAL INFORMATION:  
; APPLICANT: Brigham-Burke, Michael R.  
; APPLICANT: Young, Peter R.  
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
; FILE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2  
; CURRENT APPLICATION NUMBER: US/10/066,209  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 09/072,993  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/055,513  
; PRIOR FILING DATE: 1997-08-13  
; PRIOR APPLICATION NUMBER: 60/056,980  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/057,550  
; PRIOR FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-10-066-209-1

Query Match 87.2%; Score 1900; DB 13; Length 401;  
Best Local Similarity 85.8%; Pred. No. 3.5e-148;  
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI-IEMWTQETLPPKYLHYDPETGHQLLCKCAPGTLYLKQHCTVRRK 59  
Db 1 MNKWLCCA-LVFLDISIKWTQETLPPKYLHYDEETSHQLLCKCPPTGTYLKQHCTAKWK 59  
QY 60 TLCVPCPDHSHYTDSDWHTSDECYVCSVCKELQSVQECNRTHNRVCEBEGRYLIEFCL 119  
Db 60 TVCAPCPDHYTDSWHTSDECYVCSVCKELQSVQECNRTHNRVCEBEGRYLIEFCL 119  
QY 120 KHRSCPPGSGVVGAGTPEINTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATH 179  
Db 120 KHRSCPPGSGVVGAGTPEINTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLQKGNATH 179  
QY 180 THDNVCSGNREATKCGIDVTLCCEAFAFFRFAVPTKIIPNLSVLVDSLPGTKNVASEVER 239  
Db 180 THDNVCSGNREATKCGIDVTLCCEAFAFFRFAVPTKIIPNLSVLVDSLPGTKNVASEVER 239  
QY 240 IKRRHSSQEQTFQLLKWKHQNQDQWVKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 299  
Db 240 IKRRHSSQEQTFQLLKWKHQNQDQWVKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 299  
QY 300 ESLPGKKISPEIERTRKTKSSQEQTFQLLKWKHQNQDQWVKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 359  
Db 300 ESLPGKKISPEIERTRKTKSSQEQTFQLLKWKHQNQDQWVKIIQDIDLCESSVQRHLGHSNLTTEQLLALM 359  
QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
Db 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

## RESULT 6

US-10-105-934-2  
; Sequence 2, Application US/10105934  
; Publication No. US20020150988A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.

Holtzman, Douglas  
 TITLE OF INVENTION: NOVEL MOLECULES OF THE FTHA-070-RELATED PROTEIN FAMILY AND THE T85-RELATED PROTEIN FAMILY AND USES THEREOF  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/105,934  
 FILING DATE: 25-Mar-2002  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/062,389  
 FILING DATE: 17-APR-1998  
 APPLICATION NUMBER: 60/062,017  
 FILING DATE: 10-OCT-1997  
 APPLICATION NUMBER: 60/044,746  
 FILING DATE: 18-APR-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meiklejohn, Anita L.  
 REGISTRATION NUMBER: 35,283  
 REFERENCE/DOCKET NUMBER: 09404/051001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-8906  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 401 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-105-934-2

Query Match 87.2%; Score 1900; DB 13; Length 401;  
 Best Local Similarity 85.8%; Pred. No. 3.5e-148;  
 Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;  
 QY 1 MNKWLCCALLVLVDI-IEWTQETLPPKYLHYDPETGHQLLCKKCAPGTLYLKQHCTVRRK 59  
 DB 1 MNKLLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKKCPGPGTLYLKQHCTAKWK 59  
 QY 60 TLCVPCPDHSYDTSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119  
 DB 60 TVCAPCPDHYTDSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119  
 QY 120 KHRSCPPGSGVQAGTPERTNVCCKPDGFFSGTSSKAPCIKHTNCSTFGLLIQKNA 179  
 DB 120 KHRSCPPGSGVQAGTPERTNVCCKPDGFFSGTSSKAPCRKHTNCSVFGLLLTQKNA 179  
 QY 180 THDNVCSGNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLSDLVSLPGTKVNAESVER 239  
 DB 180 THDNVCSGNSESTQKCGIDVTLCEAFRFAVPTKFTFNWLSVLDNLPGTKVNAESVER 239  
 QY 240 IKRRHSSQEQTFQLLKLWKHQNDRDQEMVKKIIQDIDLCESSVQRHGLHSNLTTEQLLALM 299  
 DB 240 IKRQHSSEQEQTFQLLKLWKHQNKDQDIVKKIIQDIDLCESSVQRHGHANLTFEQLRSLM 299  
 QY 300 ESLPGKKISPEEIERTRKTSSEQLLKLISLRINKGDDOTLKGLMYALKHLKTSHPFK 359  
 DB 300 ESLPGKKVGAEDIEKTIKACPSDQILKLSLRINKGDDOTLKGLMHALKHSKTYHFPK 359  
 QY 360 TVTSHLRKTMRFHLHSFTMYRLYQKLFLEMIQNVQSVKISCL 401  
 DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIQNVQSVKISCL 401

QY 360 TVTSHLRKTMRFHLHSFTMYRLYQKLFLEMIQNVQSVKISCL 401  
 DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIQNVQSVKISCL 401  
 RESULT 7  
 US-10-164-592-2  
 ; Sequence 2, Application US/10164592  
 ; Publication No. US20020150989A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Greene, John W.  
 ; APPLICANT: Fleischmann, Robert D.  
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor  
 ; FILE REFERENCE: 1488.0710007  
 ; CURRENT APPLICATION NUMBER: US/10/164,592  
 ; PRIOR FILING DATE: 2002-06-10  
 ; PRIOR APPLICATION NUMBER: US 08/469,637  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR APPLICATION NUMBER: PCT/US95/03216  
 ; PRIOR FILING DATE: 1995-03-15  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 401  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-164-592-2

Query Match 87.2%; Score 1900; DB 13; Length 401;  
 Best Local Similarity 85.8%; Pred. No. 3.5e-148;  
 Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;  
 QY 1 MNKWLCCALLVLVDI-IEWTQETLPPKYLHYDPETGHQLLCKKCAPGTLYLKQHCTVRRK 59  
 DB 1 MNKLLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKKCPGPGTLYLKQHCTAKWK 59  
 QY 60 TLCVPCPDHSYDTSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119  
 DB 60 TVCAPCPDHYTDSWHTSDVCVSPVKELQSVKQECNTHNRVCECEGRYLEIEFCL 119  
 QY 120 KHRSCPPGSGVQAGTPERTNVCCKPDGFFSGTSSKAPCIKHTNCSTFGLLIQKNA 179  
 DB 120 KHRSCPPGSGVQAGTPERTNVCCKPDGFFSGTSSKAPCRKHTNCSVFGLLLTQKNA 179  
 QY 180 THDNVCSGNREATQKCGIDVTLCEAFRFAVPTKIIIPNWLSDLVSLPGTKVNAESVER 239  
 DB 180 THDNVCSGNSESTQKCGIDVTLCEAFRFAVPTKFTFNWLSVLDNLPGTKVNAESVER 239  
 QY 240 IKRRHSSQEQTFQLLKLWKHQNDRDQEMVKKIIQDIDLCESSVQRHGLHSNLTTEQLLALM 299  
 DB 240 IKRQHSSEQEQTFQLLKLWKHQNKDQDIVKKIIQDIDLCESSVQRHGHANLTFEQLRSLM 299  
 QY 300 ESLPGKKISPEEIERTRKTSSEQLLKLISLRINKGDDOTLKGLMYALKHLKTSHPFK 359  
 DB 300 ESLPGKKVGAEDIEKTIKACPSDQILKLSLRINKGDDOTLKGLMHALKHSKTYHFPK 359  
 QY 360 TVTSHLRKTMRFHLHSFTMYRLYQKLFLEMIQNVQSVKISCL 401  
 DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIQNVQSVKISCL 401

RESULT 8  
 US-10-044-674-3  
 ; Sequence 3, Application US/10044674  
 ; Publication No. US2003017510A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chew, Anne  
 ; APPLICANT: Denton, R. Rex  
 ; APPLICANT: Bieglecki, Karyn M  
 ; APPLICANT: Nandabalan, Krishnan  
 ; APPLICANT: Stephens, J. Claiborne  
 ; TITLE OF INVENTION: HAPLOTYPE OF THE TNFRSF11B GENE  
 ; FILE REFERENCE: TNFRSF11B\_MWH-0001US (CIP)

```

; CURRENT APPLICATION NUMBER: US/10/044,674
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/18803
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-674-3

Query Match      87.2%; Score 1900; DB 14; Length 401;
Best Local Similarity 85.8%; Pred. No. 3.5e-148;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI-IETWTTQETLPKYLHYDPETGHQLLCKDCAPGTYLKQHCTVRRK 59
Db 1 MNKWLCCA-LVFLDISIKWTTQETFPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWK 59
QY 60 TLCVPCPDHYSYDTSWHTSDCVYCSVPVKELQSVKQECNTHNRVCECEGRYLEIBFCL 119
Db 60 TVCAPCPDHYTDSWHTSDCLYCSVPVKELQSVKQECNTHNRVCECEGRYLEIBFCL 119
QY 120 KHRSCPPGSGVQAGTPERNTVCKCPDGFPSGETSKAPCIKHTNGSTFGLLLIQGNA 179
Db 120 KHRSCPPGFGVQAGTPERNTVCKRCPDGFFSNSTSSKAPCRKHTNGSVFGLLLTQKQNA 179
QY 180 THDNVCSGNREATQKCGIDVTLCEEAFFRAVPTKIIPNWLSVLVDSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCEEAFFRAVPTKFTPNWLSVLVLDLPGTKVNAESVER 239
QY 240 IKRHSSEQEOTFOLLKLWKHQNRDQEMVKIIQDIDLCSSVQRHGLGHSNLTTEQLLALM 299
Db 240 IKQHSSEQEOTFOLLKLWKHQNKDQDIVKKIIQDIDLCENSQRHGHANLTFEQLASLM 299
QY 300 ESLPGKKISPEETERTKTKSSSEQLLKLSLRWIKNGDQDTLKLGLMYALKHLSHTFPK 359
Db 300 ESLPGKKVGAEDIEKTKACKPSDQILKLLSLRWIKNGDQDTLKLGLMHALKHSKTYHFPK 359
QY 360 TVTHSLRKTWRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNOVQSVKISCL 401

RESULT 9
US-10-322-673-5
; Sequence 5, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      87.2%; Score 1900; DB 14; Length 401;

US-10-322-673-5
; Sequence 5, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-5

Query Match      87.2%; Score 1900; DB 14; Length 401;

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Best Local Similarity 85.8%; Pred. No. 3.5e-148;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLDI-IEWTTOETLPPKYLHYDPTGHQLLDCDCAPGTYLKQHCCTVRK 59
Db 1 MNKWLCCCA-LVFLDISIKWTQETPPKYLHYDETSQQLLDCDCPPGTYLKQHCCTAKWK 59
QY 60 TLVCPDPHSYTDSTWHTSDCYCSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCL 119
Db 60 TVCAPCPDHYTDSWHTSDCYCSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCL 119
QY 120 KHRSCPPGSGVVOAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKNA 179
Db 120 KHRSCPPGFGVVOAGTPERNTVCKKCPDGFSGTSSKAPCRKHTNCSVFGLLLTQKNA 179
QY 180 THDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNMLSVLVDLSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCCEAFRFAVPTKFTPNMLSVLVDNLPGTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKLWKHQNRODMVKKIIQIDILCESSVQRHLGHSNLTTEQLIALM 299
Db 240 IKRQHSQEQTFQLLKLWKHQNRODMVKKIIQIDILCESSVQRHIGHANLTTEQLRSLM 299
QY 300 ESLPGKISPEIERTRTKCKSSQQLKLSLWRIKNGDQDTLGLMYALKHKTSHPPK 359
Db 300 ESLPGKVGADIEKTIKACKPSQIILKLSLWRIKNGDQDTLGLMHALKHKSHTYHPPK 359
QY 360 TVTSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 11
US-10-895-676-2
; Sequence 2, Application US/10895676
; Publication No. US20050032172A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; HOLZMAN, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE FTHMA-070-
RELATED PROTEIN FAMILY AND THE T85-RELATED PROTEIN
FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/895,676
; FILING DATE: 21-Jul-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/105,934
; FILING DATE: 25-Mar-2002
; APPLICATION NUMBER: US/09/062,389
; FILING DATE: 17-APR-1998
; APPLICATION NUMBER: 60/062,017
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/044,746
; FILING DATE: 18-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/051001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
```

```
TELEFAX: 617/542-8906
TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-895-676-2

Query Match 87.2%; Score 1900; DB 17; Length 401;
Best Local Similarity 85.8%; Pred. No. 3.5e-148;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLDI-IEWTTOETLPPKYLHYDPTGHQLLDCDCAPGTYLKQHCCTVRK 59
Db 1 MNKWLCCCA-LVFLDISIKWTQETPPKYLHYDETSQQLLDCDCPPGTYLKQHCCTAKWK 59
QY 60 TLVCPDPHSYTDSTWHTSDCYCSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCL 119
Db 60 TVCAPCPDHYTDSWHTSDCYCSPVCKELQSVKQECNRTHNRVCECEGRYLEIEFCL 119
QY 120 KHRSCPPGSGVVOAGTPERNTVCKKCPDGFSGTSSKAPCIKHTNCSTFGLLLIQKNA 179
Db 120 KHRSCPPGFGVVOAGTPERNTVCKKCPDGFSGTSSKAPCRKHTNCSVFGLLLTQKNA 179
QY 180 THDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKIIIPNMLSVLVDLSLPGTKVNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCCEAFRFAVPTKFTPNMLSVLVDNLPGTKVNAESVER 239
QY 240 IKRRHSSQEQTFQLLKLWKHQNRODMVKKIIQIDILCESSVQRHLGHSNLTTEQLIALM 299
Db 240 IKRQHSQEQTFQLLKLWKHQNRODMVKKIIQIDILCESSVQRHIGHANLTTEQLRSLM 299
QY 300 ESLPGKISPEIERTRTKCKSSQQLKLSLWRIKNGDQDTLGLMYALKHKTSHPPK 359
Db 300 ESLPGKVGADIEKTIKACKPSQIILKLSLWRIKNGDQDTLGLMHALKHKSHTYHPPK 359
QY 360 TVTSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401
Db 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

RESULT 12
US-09-062-113-5
; Sequence 5, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Teeta, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/062,113  
FILING DATE: 17-APR-1998  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 54977/1995  
FILING DATE: 20-FEB-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 207508/1995  
FILING DATE: 21-JUL-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/00374  
FILING DATE: 20-FEB-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,004  
FILING DATE: 20-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MOORE, Ronda P.  
REGISTRATION NUMBER: 44,244  
REFERENCE/DOCKET NUMBER: FJN-060DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..380  
OTHER INFORMATION: /note= "(OCIF protein)"  
NAME/KEY: Peptide  
LOCATION: -21..0  
OTHER INFORMATION: /note= "(signal peptide)"  
US-09-062-113-5

Query Match 87.0%; Score 1895; DB 9; Length 401;  
Best Local Similarity 85.6%; Pred. No. 8.9e-148;  
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;  
Qy 1 MNKWLCCALLVLDI-IEWTTOETLPKYLHYDPETHGOLLCDCAPGYLKHCHTVRRK 59  
Db 1 MNLLCCA-LVFLDISIKWTQETFPKYLHYDETSQHLCDKCPGTYLKHCHTAKWK 59  
Qy 60 TLCVPCPDHSDYSDSWHTSDEVCVSPVKELQSVKQECNTHNRVCEBGRYLEIEFCL 119  
Db 60 TVCAPCPDHYTDSWHTSDECLYCSVPKELQYVKQECNTHNRVCEBGRYLEIEFCL 119  
Qy 120 KHRSCPPGSGVVOAGTPERNTVCKCPDGFPGSTSSKAPCIKHTNCSSTGELLIIQKNA 179  
Db 120 KHRSCPPGFGVVOAGTPERNTVCKCPDGFPGFNSNETSSKAPCRKHTNCSVFGLLLITQKNA 179  
Qy 180 THDNVCSGNREATQKCGIDVTLCSEAFREAVPTKIIIPNWLVLVDSLPGTKVNAESVER 239  
Db 180 THDNICSGNSESTQKCGIDVTLCSEAFREAVPTKFTFNWLVLVDNLPGTKVNAESVER 239  
Qy 240 IKRHSQEQOTFOLLKWLKHQNRQEMVKIIQDIDICSSVQRHLGHSNLTTEQLLALM 299  
Db 240 IKRHSQEQOTFOLLKWLKHQNKQDQIVKKIIQDIDICENSQRHIGHANLTFEQLASLM 299  
Qy 300 ESLPGKKISPEIERTRTKCSSEQLLKLSLMRIKNGDQDTLKGMLYALKHKTSHPPK 359  
Db 300 ESLPGKKVGAEDIEKTIKACKPSQILKLLSLMRIKNGDQDTLKGMLHAKHKSITYHPPK 359  
Qy 360 TVTHSLAKTRWPLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401  
Db TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

Db 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401  
RESULT 13  
US-10-183-091-1  
Sequence 1, Application US/10183091  
Publication No. US20030045456A1  
GENERAL INFORMATION:  
APPLICANT: Yamamoto, Shinichi  
APPLICANT: Okada, Junichi  
APPLICANT: Kurihara, Atsushi  
APPLICANT: Numazawa, Taku  
APPLICANT: Kondo, Junichi Tenda, Bisuke  
APPLICANT: Mochizuki, Shinichi  
APPLICANT: Nishi, Hirotsuka  
APPLICANT: Miyazaki, Hideki  
TITLE OF INVENTION: A complex comprising OCIF and polysaccharide  
FILE REFERENCE: 02280/HG  
CURRENT APPLICATION NUMBER: US/10/183,091  
CURRENT FILING DATE: 2002-06-27  
PRIOR APPLICATION NUMBER: JP 2001-198985  
PRIOR FILING DATE: 2001-06-29  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 401  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (-21)..(-1)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: (+1)..(+380)  
OTHER INFORMATION:  
US-10-183-091-1

Query Match 87.0%; Score 1895; DB 14; Length 401;  
Best Local Similarity 85.6%; Pred. No. 8.9e-148;  
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;  
Qy 1 MNKWLCCALLVLDI-IEWTTOETLPKYLHYDPETHGOLLCDCAPGYLKHCHTVRRK 59  
Db 1 MNLLCCA-LVFLDISIKWTQETFPKYLHYDETSQHLCDKCPGTYLKHCHTAKWK 59  
Qy 60 TLCVPCPDHSDYSDSWHTSDEVCVSPVKELQSVKQECNTHNRVCEBGRYLEIEFCL 119  
Db 60 TVCAPCPDHYTDSWHTSDECLYCSVPKELQYVKQECNTHNRVCEBGRYLEIEFCL 119  
Qy 120 KHRSCPPGSGVVOAGTPERNTVCKCPDGFPGSTSSKAPCIKHTNCSSTGELLIIQKNA 179  
Db 120 KHRSCPPGFGVVOAGTPERNTVCKCPDGFPGFNSNETSSKAPCRKHTNCSVFGLLLITQKNA 179  
Qy 180 THDNVCSGNREATQKCGIDVTLCSEAFREAVPTKIIIPNWLVLVDSLPGTKVNAESVER 239  
Db 180 THDNICSGNSESTQKCGIDVTLCSEAFREAVPTKFTFNWLVLVDNLPGTKVNAESVER 239  
Qy 240 IKRHSQEQOTFOLLKWLKHQNRQEMVKIIQDIDICSSVQRHLGHSNLTTEQLLALM 299  
Db 240 IKRHSQEQOTFOLLKWLKHQNKQDQIVKKIIQDIDICENSQRHIGHANLTFEQLASLM 299  
Qy 300 ESLPGKKISPEIERTRTKCSSEQLLKLSLMRIKNGDQDTLKGMLYALKHKTSHPPK 359  
Db 300 ESLPGKKVGAEDIEKTIKACKPSQILKLLSLMRIKNGDQDTLKGMLHAKHKSITYHPPK 359  
Qy 360 TVTHSLAKTRWPLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401  
Db TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401  
RESULT 14  
US-10-364-045-1

; Sequence 1, Application US/10364045  
; Publication No. US20030139325A1

## ; GENERAL INFORMATION:

; APPLICANT: Yamamoto, Shinichi  
; APPLICANT: Okada, Junichi  
; APPLICANT: Kurihara, Acsuehi  
; APPLICANT: Numazawa, Taku  
; APPLICANT: Kondo, Junichi  
; APPLICANT: Mochizuki, Shinichi  
; APPLICANT: Nishi, Hirotaka  
; APPLICANT: Miyazaki, Hideki  
; TITLE OF INVENTION: A complex comprising OCIF and polysaccharide

; FILE REFERENCE: 02280/HG

; CURRENT APPLICATION NUMBER: US/10/364,045

; CURRENT FILING DATE: 2003-02-11

; PRIOR APPLICATION NUMBER: US/10/183,091

; PRIOR FILING DATE: 2002-06-27

; PRIOR APPLICATION NUMBER: JP 2001-198985

; PRIOR FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 401

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (-21)..(-1)

; OTHER INFORMATION:

; FEATURE:

; NAME/KEY: mat\_peptide

; LOCATION: (\*1)..(\*380)

; OTHER INFORMATION:

US-10-364-045-1

Query Match 87.0%; Score 1895; DB 14; Length 401;

Best Local Similarity 85.6%; Pred. No. 8.9e-148;

Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI - IEWTTQETLPKYLHYDPTGHQLCDKCAPGYLKQHCTVRRK 59

Db 1 MNLLCCA - LVFLDISIKWTQETFPKYLHYDEETSHQLCDKCPGGYLYLKQHCTAKWK 59

QY 60 TLVCPCPDHSDYDTSWHTSDECVYCSVKELQSVKQECNRTNHRVCECEEGRYLIEFCL 119

Db 60 TVCAPCPDHYTDSWHTSDECLYCSVKELQSVKQECNRTNHRVCECEEGRYLIEFCL 119

QY 120 KHRSCPPGSGVVQAGTPERTNVCCKCPDGFSGSETSSKAPCIKHTNCSTFGILLITQKNA 179

Db 120 KHRSCPPGSGVVQAGTPERTNVCCKCPDGFSGSETSSKAPCRKHTNCSTFGILLITQKNA 179

QY 180 THDNVCSGNREATQCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVDSLPGTKVNAESVER 239

Db 180 THDNVCSGNSESTQCGIDVTLCCEAFFRFAVPTKFTPNWLSVLDNLPGTKVNAESVER 239

QY 240 IKRRSSQEQTFQLLKLWKHQNDRDQEMVKIIQDIDLCSSVQRHGHNSLNTTEQLLALM 299

Db 240 IKRQSSQEQTFQLLKLWKHQNDRDQEMVKIIQDIDLCSSVQRHGHNSLNTTEQLRLSLM 299

QY 300 ESLPGKKISPEIERTRTKCSSEOLLKLSLWRIKNGDQDTLKGIMVALKHLKTSHPK 359

Db 300 ESLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGIMVALKHLKTSHPK 359

QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Db 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

RESULT 15

US-10-232-858-5

; Sequence 5, Application US/10232858

; Publication No. US20030153048A1

; GENERAL INFORMATION:

; APPLICANT: GOTO, Masaaki  
; APPLICANT: TSUDA, Eisuke  
; APPLICANT: MOCHIZUKI, Shin'ichi  
; APPLICANT: YANO, Kazuki  
; APPLICANT: KOBAYASHI, Fumie  
; APPLICANT: SHIMA, No. US20030153048A1uuyuki  
; APPLICANT: YASUDA, Hisataka  
; APPLICANT: NAKAGAWA, No. US20030153048A1uaki  
; APPLICANT: MORINAGA, Tomonori  
; APPLICANT: UEDA, Masatsugu  
; APPLICANT: HIGASHIO, Kanji

; TITLE OF INVENTION: No. US20030153048A1el Proteins and Methods for Producing the Prote

; FILE REFERENCE: 16991.004

; CURRENT APPLICATION NUMBER: US/10/232,858

; CURRENT FILING DATE: 2002-09-03

; PRIOR APPLICATION NUMBER: PCT/JP96/00374

; PRIOR FILING DATE: 1996-02-20

; PRIOR APPLICATION NUMBER: 08/915,004

; PRIOR FILING DATE: 1997-08-20

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 401

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-232-858-5

Query Match 87.0%; Score 1895; DB 14; Length 401;

Best Local Similarity 85.6%; Pred. No. 8.9e-148;

Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;

QY 1 MNKWLCCALLVLLDI - IEWTTQETLPKYLHYDPTGHQLCDKCAPGYLKQHCTVRRK 59

Db 1 MNLLCCA - LVFLDISIKWTQETFPKYLHYDEETSHQLCDKCPGGYLYLKQHCTAKWK 59

QY 60 TLVCPCPDHSDYDTSWHTSDECVYCSVKELQSVKQECNRTNHRVCECEEGRYLIEFCL 119

Db 60 TVCAPCPDHYTDSWHTSDECLYCSVKELQSVKQECNRTNHRVCECEEGRYLIEFCL 119

QY 120 KHRSCPPGSGVVQAGTPERTNVCCKCPDGFSGSETSSKAPCIKHTNCSTFGILLITQKNA 179

Db 120 KHRSCPPGSGVVQAGTPERTNVCCKCPDGFSGSETSSKAPCRKHTNCSTFGILLITQKNA 179

QY 180 THDNVCSGNREATQCGIDVTLCCEAFFRFAVPTKIIIPNWLSDLVDSLPGTKVNAESVER 239

Db 180 THDNVCSGNSESTQCGIDVTLCCEAFFRFAVPTKFTPNWLSVLDNLPGTKVNAESVER 239

QY 240 IKRRSSQEQTFQLLKLWKHQNDRDQEMVKIIQDIDLCSSVQRHGHNSLNTTEQLLALM 299

Db 240 IKRQSSQEQTFQLLKLWKHQNDRDQEMVKIIQDIDLCSSVQRHGHNSLNTTEQLRLSLM 299

QY 300 ESLPGKKISPEIERTRTKCSSEOLLKLSLWRIKNGDQDTLKGIMVALKHLKTSHPK 359

Db 300 ESLPGKKVGAEDIEKTIKACPSDQILKLSLWRIKNGDQDTLKGIMVALKHLKTSHPK 359

QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401

Db 360 TVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 401

Search completed: March 8, 2005, 15:16:01

Job time : 62.5885 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.3429 Seconds  
(without alignments)  
2360.831 Million cell updates/sec

Title: US-09-389-782a-2  
Perfect score: 2179  
Sequence: 1 MNKWLCCALLVLDIIETW.....QKLPLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	314	14.4	459	2 148854	gene murine tumor
2	312	14.3	461	1 A35356	tumor necrosis fac
3	312	14.3	474	2 B38634	tumor necrosis fac
4	300.5	13.8	651	2 JC7705	death receptor-6 -
5	270	12.4	305	2 A46476	B cell-associated
6	261	12.0	277	2 A60771	B-cell activation
7	244	11.2	435	2 I54182	tumor necrosis fac
8	233.5	10.7	325	2 B43692	T2 protein - rabbi
9	220	10.1	326	1 GQVZML	T2 protein - myxom
10	217	10.0	349	2 D36858	gene G4R protein -
11	216	9.9	349	2 D72175	G2R protein - vari
12	215.5	9.9	348	2 T28623	hypothetical prote
13	199	9.1	427	1 GQHUN	nerve growth facto
14	197.5	9.1	425	1 A26431	nerve growth facto
15	184	8.4	416	1 JN0006	nerve growth facto
16	182	8.4	335	2 A40036	apoptosis-meditin
17	179.5	8.2	314	2 I37383	FAS soluble protei
18	177	8.1	256	2 B32393	T-cell antigen 4-1
19	167	7.7	255	2 I38426	lymphocyte activat
20	165.5	7.6	461	2 JC4302	tumor necrosis fac
21	163	7.5	271	2 S12783	OX40 antigen precu
22	161.5	7.4	454	1 GQMT11	tumor necrosis fac
23	160	7.3	465	1 GQHTU1	tumor necrosis fac
24	153	7.0	461	1 GQRT11	tumor necrosis fac
25	152.5	7.0	272	2 I48700	gene ox40 protein
26	151	6.9	272	2 I37552	OX40 homolog - hum
27	147.5	6.8	324	2 JC2395	Fas antigen precur
28	143	6.6	327	2 A46484	apoptosis-meditin
29	142.5	6.5	2823	2 F87908	protein T22A3.8 [1

30	142.5	6.5	2823	2 T23064	hypothetical prote
31	142.5	6.5	3102	2 T43291	laminin alpha chai
32	139	6.4	595	2 A42086	CD30 antigen precu
33	137.5	6.3	899	2 G02428	subtilisin-like pr
34	137.5	6.3	915	2 JC6148	subtilisin-like pr
35	133	6.1	1786	1 MMHUB1	laminin beta-1 cha
36	131.5	6.0	260	1 A46517	CD27 antigen precu
37	128.5	5.9	1252	2 S36016	occyet wall protei
38	128.5	5.9	1790	1 MMFPB1	laminin beta-1 cha
39	126.5	5.8	1548	2 S34583	serine proteinase
40	125	5.7	1680	2 A43434	furin (EC 3.4.21.7
41	122	5.6	1372	2 T25933	hypothetical prote
42	120.5	5.5	250	1 A49053	CD27 antigen precu
43	120.5	5.5	2918	2 A54105	fibrillin-2 precur
44	119.5	5.5	1639	1 MMFPB2	laminin gamma-1 ch
45	119	5.5	1364	2 T00250	MEGF2 protein - hu

ALIGNMENTS

RESULT 1

I48854  
gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48854  
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A;Reference number: I48854; MUID:95178848; PMID:7873884  
A;Accession: I48854  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-459 <RES>  
A;Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:q433830; PIDN:CAA53981.1; PID:q43383;  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 14.4%; Score 314; DB 2; Length 459;  
Best Local Similarity 34.6%; Pred. No. 3.7e-14;  
Matches 66; Conservative 20; Mismatches 79; Indels 26; Gaps 4;

Qy	18	WTQETLPKYL--HYDPTGH-----QLLCKCAPGYLKHQCTVRRKTL	62
Db	2	WATGHTVPAQVVLTPYKPEPGYEQISQEVYDRKAQMCACPPGQVYKFCNKTS	61
Qy	63	VPCPDHSYTDWHTSDCVYSPVKELQSVKQCNTRNVRVCEEGRYLEIEF----	117
Db	62	ADCEASMYTQVMNQFRTCLSSSSCSSTQVETRACTQQRNVCAAGRYCALUKTH	121
Qy	118	--CLKHRSPPGSGVQAGTPERTVCKPCDGFSGSETSSKAPCIKHTNCSTFGLLI	175
Db	122	RQCMRLSKGPGFGVASSRAPNGVLCACAPCTFSDTTSSTVDCRPHRCS----	177
Qy	176	KGNAHDNVCS 186	
Db	178	PGNASTDAVCA 188	

RESULT 2

A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerry, R.; Dower, S.K.  
Science 248, 1019-1023, 1990  
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A;Reference number: A35356; MUID:90260639; PMID:2160731  
A;Accession: A35356  
A;Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: UNIPROT:P20333; GB:M32315; NID:G189185; PIDN:AAA59929.1; PID:G189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring  
A:Reference number: A36475; MUID:91045991; PMID:2172983  
A:Accession: A36475  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36755.1; PID:G339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690; PMID:1966549  
A:Accession: A48416  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:G235648; PIDN:AAB19824.1; PID:G235649  
A>Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)  
R:Heiler, K.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of two distinct tumor necrosis factor receptors  
A:Reference number: A36007; MUID:90349572; PMID:2166946  
A:Accession: A36007  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEU>  
A:Cross-references: GB:M35857; NID:G339751; PIDN:AAA63262.1; PID:G339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors  
A:Reference number: A23666; MUID:91056048; PMID:2173696  
A:Accession: A23666  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOB>  
R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct tumor necrosis factor receptors  
A:Reference number: A35010; MUID:90110215; PMID:2153136  
A:Accession: B35010  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kunert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of the human TNF receptor  
A:Reference number: I38094; MUID:95121934; PMID:7821811  
A:Accession: I38094  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:125914; OMIM:191191  
A:Map position: 1p36.2-1p36.2  
A:Introns: 26/3  
A>Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology <SIG>  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:40-76/Domain: NGF receptor repeat homology <NG1>  
F:78-119/Domain: NGF receptor repeat homology <NG2>  
F:120-162/Domain: NGF receptor repeat homology <NG3>  
F:164-201/Domain: NGF receptor repeat homology <NG4>  
F:262-279/Domain: transmembrane #status predicted <TMN>  
F:280-461/Domain: intracellular #status predicted <INT>  
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 312; DB 1; Length 461;  
Best Local Similarity 34.7%; Pred. No. 5.1e-14;  
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;  
QY 8 ALLVLLDIIEWTQTETLPK--YLHYDPETGH-----QLLCDKCAFGTYLKQH 53  
DB 9 ALAVGLEL--WAAAHALPAQVAFTYAPGPGSTCLREYDYDTQAMCCSKSPQHAQVF 66  
QY 54 CTVRKTLVCPDPHSYTDSDHSTDECYVSPVCKELQSVKQECNTRNHRVCEEGRYL 113  
DB 67 CTKTSDFVDCSDCESTYTLQWNVPECLSCGSRSSDQVETQACTREQNRICTRCPGWYC 126  
QY 114 EI-----EFLKHSRCPGSGVVOAGTPTERTVCKKCPDGFPGSTSSKAPCIKHTNCS 167  
DB 127 ALSKQEGCRLCAPLKRCPGFGVAPGTETSDVVVCKPCAPGTFSNTTSDICRPHQICN 186  
QY 168 TFGLLLIQKGNATHDNYCS 186  
DB 187 VVAI-----PGNASMDAVCT 201  
RESULT 3  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: B38634; A40254; S54816  
R:Levis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors  
A:Reference number: A38634; MUID:91187885; PMID:1849278  
A:Accession: B38634  
A:Molecule type: mRNA  
A:Residues: 1-474 <LEW>  
A:Cross-references: UNIPROT:P25119; GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828  
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkinson, M. Mol. Cell. Biol. 11, 3020-3026, 1991  
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor  
A:Reference number: A40254; MUID:91246168; PMID:1645445  
A:Accession: A40254  
A:Molecule type: mRNA  
A:Residues: 1-474 <GOO>  
A:Cross-references: GB:M60469; NID:G199827; PIDN:AAA39752.1; PID:G199828  
R:Kisssonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y. Submitted to the EMBL Data Library, May 1995  
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A:Reference number: S54816  
A:Accession: S54816  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-22 <KIS>  
A:Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044  
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology <SIG>  
C:Keywords: cytokine receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F:40-77/Domain: NGF receptor repeat homology <NG1>  
F:79-120/Domain: NGF receptor repeat homology <NG2>  
F:166-203/Domain: NGF receptor repeat homology <NG4>  
Query Match 14.3%; Score 312; DB 2; Length 474;  
Best Local Similarity 34.3%; Pred. No. 5.3e-14;  
Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;  
QY 5 LCCALLVLDIIEWTQTETLPKYL--HYDPTGH-----QLLCDKCAFGTY 49  
DB 6 LWALVFEQL--WATGHTVPAQVLTVPKPGVGCQISQBYDRKAQMCCKACPPGY 63  
QY 50 LKQHCVTVRKTLVCPDPHSYTDSDHSTDECYVSPVCKELQSVKQECNTRNHRVCEEE 109  
DB 64 VKHFCNKTSDTVCAECEASMYTQVMNQFRTCLSCSSSTTDDQVETRACTKQNRVCAEEA 123

[illegible]

A;Residues: 1-305 <TOR>  
A;Cross-references: UNIPROT:P27512; GB:M93312; NID:g1553058  
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)  
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0  
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992  
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A;Reference number: A46515; MUID:93094586; PMID:1281194  
A;Accession: A46515  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-287,'LV'<GRI>  
A;Cross-references: GB:M93312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; NJ  
A;Experimental source: BALB/c, liver  
A;Note: sequence extracted from NCBI backbone (NCBIPI:120357)  
C;Comment: For an alternative splice form, see PIR:A46515.  
C;Comment: For an alternative splice form, see PIR:A46476.  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: alternative splicing; transmembrane protein  
F;I05-144/Domain: NGF receptor repeat homology <NGF>

Query Match 12.4%; Score 270; DB 2; Length 305;  
Best Local Similarity 34.5%; Pred. No. 2.5e-11;  
Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

Qy 27 KYLHYDPETGHQLLCDKCAPGYLYKHQCTVRRKTLVPCPDHSYTDMSHTSDEC---VVVC 83  
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 30 QYLH-DQG-----CCDLQCQPSRLTSHCTALEKTQCHPCDSGEFSQAQNNREIRCHQHRC 83

Qy 84 SPVKELQSIVKQECNRTHNVCEEBRYL---ELEPCLKHRSCTPGSGVQAGTPERT 140  
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 84 EP--NQGLRVKKEGTABSDDTVCTCKEGHQTSKDCAEAQHTPCIPGFGWEMATETDT 141

Qy 141 VCKKCPDGFSGEFTSSKAPCIKHNKSTFGLLLIQGNATHDNVC 185  
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 142 VCHEPCPVGFNSQSSLFEKCYPTWSCDKXNLVLQKGSQTNVIC 186

RESULT 6  
A60771  
N-cell activation protein CD40 precursor - human  
B;Alternate names: B-cell surface antigen Bp50  
C;Species: Homo sapiens (man)  
C;Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: S04460; A60771  
R;Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A;Reference number: S04460; MUID:89356608; PMID:2475341  
A;Accession: S04460  
A;Molecule type: mRNA  
A;Residues: 1-277 <STA>  
A;Cross-references: UNIPROT:P25942; EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851  
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A;Reference number: A60771; MUID:89093941; PMID:2463309  
A;Accession: A60771  
A;Molecule type: protein  
A;Residues: 21-50 <BRA>  
A;Experimental source: Burkitt lymphoma cell line Raji  
C;Genetics:  
A;Gene: GDB:CD40  
A;Cross-references: GDB:215268; OMIM:109535  
A;Map position: 20q12-20q13.2  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F;I1-20/Domain: signal sequence #status predicted <SIG>  
F;I21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F;I21-193/Domain: extracellular #status predicted <EXT>  
F;I194-215/Domain: transmembrane #status predicted <TM>  
F;I216-277/Domain: intracellular #status predicted <CYT>  
F;I153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;I153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 10  
36858  
          ene G4R protein - variola virus  
          ;Alternate names: B28R protein (COP)  
          ;Species: variola virus

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: D36858; S46888; S32385; S35987  
R;Blinov, V.M.  
Submitted to GenBank, November 1992  
A;Reference number: A36859  
A;Accession: D36858  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-349 <BLI>  
A;Cross-references: EMBL:P34015; GB:X69198; MID:G456758; PIDN:CAA49137.1; PID:G457087  
A;Experimental source: strain India-1967, sep. major, isolate Ind3  
R;Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov  
submitted to the EMBL Data Library, April 1992  
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P  
A;Reference number: S46868  
A;Accession: S46888  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-349 <COL>  
A;Cross-references: EMBL:X67117; MID:G516428; PIDN:CAA47540.1; PID:G516449  
A;Experimental source: strain India-1967, isolate Ind3  
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.  
FEBS Lett. 319, 80-83, 1993  
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective  
A;Reference number: S32385; MUID:93202281; PMID:8384129  
A;Accession: S32385  
A;Molecule type: DNA  
A;Residues: 31-168 <SHC>  
A;Cross-references: EMBL:X69198  
A;Experimental source: strain India-1967, sep. major  
C;Gene: G4R  
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology  
F;32-66/Domain: NGF receptor repeat homology <NGF>  
F;68-109/Domain: NGF receptor repeat homology <NG2>  
F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 10.0%; Score 217; DB 2; Length 349;  
Best Local Similarity 23.2%; Pred. No. 1.2e-07;  
Matches 92; Conservative 51; Mismatches 169; Indels 84; Gaps 17;

QY 4 WLCCALLVLDIETWTQETLPKYLHYDPE-TGHQLLCDKCAPGTYLKQHCTVRRKTLG 62  
DB 11 FLSCIIINGRDAAPYT-----PENGKCKDTEYKRHNLCCLSCPPGTIVASRLCDSKTNWTC 65  
QY 63 VPCPDHSYTDSWHTSDECVYCVKELQSVKQECNTHNRVCEBEGRYLEI-----E 116  
DB 66 TPCGSGFTSRNNHLPACLSCNGRCNSQVETRSCNTHNRICECSPGYCYLLKGGSSGCK 125  
QY 117 FCLKHSRCPGSGVVOAGTPERNTVCKKCPDGFSGFSETSKAPCIKHTNCSTFGLLIQ- 175  
DB 126 ACVSQTKCGIGYG-VSGHTSVGDVICSPPCGFTGTVSHVSADKCEPVN-NTFNVIDVEI 183  
QY 176 KGNATHNVCSGNREATQKGDIVTLCEBAFFPAVPTKIIPNWLVSVDLSLPGTKVNAE 235  
DB 184 TLYPNDTSCT-----RTTTGLSE-----SILTSEL----- 210  
QY 236 SVERIKRRHS-----EQTFQLLK-----LWKHQRDOEMVKKIIQDIDLCESSVQRH 284  
DB 211 ---TITWNHTDCNPVREYFVSVLNKVATSGFTGGENRYQNIK-----VCTLNFEIK 260  
QY 285 LGHSNLTTEQLLALMESLPCKKISPEIERTRKTSKSEQLLKLSLWRKNGDQDTLKG 344  
DB 261 CNKNGSSFQKLTAKND--DGMMSHSETVTLAGDCLSSVDIYILSYNTNAQDYETDTIS- 317  
QY 345 LMVALKHL--KTSHPF-----KTVTHSLRKTMRFL 372  
DB 318 --YRVGNVLDDSHMPGSCDIHKLIITS--KPTRFL 349

RESULT 12  
T28623  
hypothetical protein G2R - variola major virus  
C;Species: variola major virus  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T28623  
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin  
Nature 366, 748-751, 1993  
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus  
A;Reference number: Z20488; MUID:94088747; PMID:8264798  
A;Accession: T28623  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-348 <WAS>  
A;Cross-references: UNIPROT:P34015; EMBL:L22579; MID:G623595; PIDN:AAA60933.1; PID:G4391  
A;Experimental source: strain Bangladesh 1975  
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 9.9%; Score 215.5; DB 2; Length 348;  
Best Local Similarity 23.1%; Pred. No. 1.6e-07;  
Matches 87; Conservative 47; Mismatches 156; Indels 87; Gaps 16;

QY 31 YDPETG-----HQLLCDKCAPGTYLKQHCTVRRKTLGVCPDHSYTDSWHTSDECV 81

C;Species: variola minor virus  
C;Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 09-Jul-2004  
C;Accession: D72175  
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopat  
submitted to GenBank, March 1998  
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor  
A;Reference number: A72150  
A;Accession: D72175  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-349 <SHC>  
A;Cross-references: UNIPROT:P34015; GB:Y16780; MID:G5830555; PIDN:CAB54798.1; PID:G58307  
A;Experimental source: strain Garcia-1966  
C;Genetics:  
A;Gene: G2R  
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 9.9%; Score 216; DB 2; Length 349;  
Best Local Similarity 23.2%; Pred. No. 1.5e-07;  
Matches 92; Conservative 51; Mismatches 169; Indels 84; Gaps 17;

QY 4 WLCCALLVLDIETWTQETLPKYLHYDPE-TGHQLLCDKCAPGTYLKQHCTVRRKTLG 62  
DB 11 FLSCIIINGRDAAPYT-----PENGKCKDTEYKRHNLCCLSCPPGTIVASRLCDSKTNWTC 65  
QY 63 VPCPDHSYTDSWHTSDECVYCVKELQSVKQECNTHNRVCEBEGRYLEI-----E 116  
DB 66 TPCGSGFTSRNNHLPACLSCNGRCNSQVETRSCNTHNRICECSPGYCYLLKGGSSGCK 125  
QY 117 FCLKHSRCPGSGVVOAGTPERNTVCKKCPDGFSGFSETSKAPCIKHTNCSTFGLLIQ- 175  
DB 126 ACVSQTKCGIGYG-VSGHTSVGDVICSPPCGFTGTVSHVSADKCEPVN-NTFNVIDVEI 183  
QY 176 KGNATHNVCSGNREATQKGDIVTLCEBAFFPAVPTKIIPNWLVSVDLSLPGTKVNAE 235  
DB 184 TLYPNDTSCT-----RTTTGLSE-----SILTSEL----- 210  
QY 236 SVERIKRRHS-----EQTFQLLK-----LWKHQRDOEMVKKIIQDIDLCESSVQRH 284  
DB 211 ---TITWNHTDCNPVREYFVSVLNKVATSGFTGGENRYQNIK-----VCTLNFEIK 260  
QY 285 LGHSNLTTEQLLALMESLPCKKISPEIERTRKTSKSEQLLKLSLWRKNGDQDTLKG 344  
DB 261 CNKNGSSFQKLTAKND--DGMMSHSETVTLAGDCLSSVDIYILSYNTNAQDYETDTIS- 317  
QY 345 LMVALKHL--KTSHPF-----KTVTHSLRKTMRFL 372  
DB 318 --YRVGNVLDDSHMPGSCDIHKLIITS--KPTRFL 349

RESULT 12  
T28623  
hypothetical protein G2R - variola major virus  
C;Species: variola major virus  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T28623  
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin  
Nature 366, 748-751, 1993  
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus  
A;Reference number: Z20488; MUID:94088747; PMID:8264798  
A;Accession: T28623  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-348 <WAS>  
A;Cross-references: UNIPROT:P34015; EMBL:L22579; MID:G623595; PIDN:AAA60933.1; PID:G4391  
A;Experimental source: strain Bangladesh 1975  
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 9.9%; Score 215.5; DB 2; Length 348;  
Best Local Similarity 23.1%; Pred. No. 1.6e-07;  
Matches 87; Conservative 47; Mismatches 156; Indels 87; Gaps 16;

QY 31 YDPETG-----HQLLCDKCAPGTYLKQHCTVRRKTLGVCPDHSYTDSWHTSDECV 81

Db 24 YTPNGKCKDTEYKRNLCCLSPGPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACL 83  
QY 82 YCSPVCKELQVQKQECNTHNRVCECEGRYLEI-----EFCLEKHSRPPGSGVVOAGT 135  
Db 84 SCNGRCNSQVFRSCNTHNRICECPGYCLLKSSGCKACVQTKGIGVG-VSGHT 142  
QY 136 PERNTVCKCPDGGFFGSETSSKAPCIKHNCSTFGLLLIQ-KGNATHDNVCSGNREATOK 194  
Db 143 SVGDVTCPCGFGTYGHTVSSADKCEPVFN-NTFNVIDVEITLYPVNDTSCT-----RTTT 197  
QY 195 CGIDVTLCBEAFRFAVPYKIIIPWLSVLVDSLPGTKVAESVERIKRRHS-----QEQ 249  
Db 198 TGLSE-----SILTSEL-----TITMHTDCNPVREE 225  
QY 250 TFOCLK-----LWKHQRNDQEMVKKIIQIDILCESSVORHLGHSNLTTEQLLALMESLP 303  
Db 226 YFSVLNKAIVSGFTGENRYQNIK-----VCTLNFIKCNKNGSSFKQLTKAKND-- 276  
QY 304 GKKSPEIERTKTKCSSEQLKLRLWIRKNGDDOTLKGLMYALKHL--KTSHP-- 358  
Db 277 DGMMSHSETVTLAGDCLSSVDIYLYSNTNAQDYETDTIS---YRVGNVLDDDDSHMPGSC 333  
QY 359 ---KTVTHSLRKTMREL 372  
Db 334 NIHKPITNS--KPTREL 348

RESULT 13  
GOHUN  
nerve growth factor receptor precursor, low affinity [validated] - human  
N:Alternate names: NGF receptor  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
R:Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
Cell 47, 545-554, 1986  
A:Title: Expression and structure of the human NGF receptor.  
A:Reference number: A25218; MUID:87051725; PMID:3022937  
A:Accession: A25218  
A:Molecule type: mRNA  
A:Cross-references: 1-427 <JOH>  
R:Marano, N.; Dietschold, B.; Earley Jr., J.J.; Schattman, G.; Thompson, S.; Grob, P.; J. Neurochem. 48, 225-232, 1987  
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
A:Reference number: A60204; MUID:87085574; PMID:3025363  
A:Accession: A60204  
A:Molecule type: protein  
A:Residues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>  
A:Experimental source: melanoma cell line A875  
A:Note: This sequence has been corrected by a note added in proof to follow the nucleotide  
R:Visavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
Arch. Biochem. Biophys. 294, 244-252, 1992  
A:Title: Structural domains of the extracellular domain of human nerve growth factor  
A:Reference number: S21689; MUID:92198017; PMID:1372492  
A:Accession: S21689  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 183-208 <VIS>  
R:Sehgal, A.; Patil, N.; Chao, M.  
Mol. Cell. Biol. 8, 3160-3167, 1988  
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor  
A:Reference number: I57638; MUID:89096903; PMID:2850481  
A:Accession: I57638  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-22 <RES>  
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA3363.1; PID:g189207  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C:Comment: This protein is thought to form a high-affinity receptor when it associates w  
C:Comment: This receptor undergoes both N- and O-linked glycosylation.

C:Genetics:  
A:Gene: GDB:NGFR  
A:Cross-references: GDB:120234; OMIM:162010  
A:Map position: 17q21-17q22  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
F:1-28/Domain: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t  
F:29-427/Product: nerve growth factor receptor #status predicted <SIG>  
F:29-427/Domain: extracellular #status predicted <EXT>  
F:32-65/Domain: NGF receptor repeat homology <NG1>  
F:67-108/Domain: NGF receptor repeat homology <NG2>  
F:109-147/Domain: NGF receptor repeat homology <NG3>  
F:149-189/Domain: NGF receptor repeat homology <NG4>  
F:197-248/Region: serine/threonine-rich  
F:251-272/Domain: transmembrane #status predicted <TRM>  
F:273-427/Domain: intracellular #status predicted <INT>  
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 199; DB 1; Length 427;  
Best Local Similarity 31.7%; Pred. No. 2.7e-06;  
Matches 52; Conservative 25; Mismatches 71; Indels 16; Gaps 6;  
QY 9 LILVLDIIEWTTOETLPPKYLHYDBETHQLLCKDCAPGYLKQHTVRRKTLVCVCPDH 68  
Db 17 LLLLLGSLGGAKAEACPTGLYTHSGE-----CCKACNLGEGVAQPCGA-NQTVCEPCLDS 70  
QY 69 -SYTDSWHTSDCVYCSVPCKELQSVKQECNTHNRVCECEGRYLE-----IEFCLKHR 122  
Db 71 VTFSDVVSATPECKPCTE-CVGLQSMAPCVADDAVCECAYGYQDETTRGCEAC---R 126

QY 123 SCPGSGVVOAGTTPERTNVCKKCPDGGFFGSETSSKAPCIKHNTNC 166  
Db 127 VCEAGSLGVSCQDKQNTVCBPCDGTYSDEANHVDPCLPCTVC 170

RESULT 14  
A26431  
nerve growth factor receptor precursor, low affinity - rat  
N:Alternate names: NGF receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A26431; PHI229  
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
Nature 325, 593-597, 1987  
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
A:Reference number: A26431; MUID:87115859; PMID:3027580  
A:Accession: A26431  
A:Molecule type: mRNA  
A:Residues: 1-425 <RAD>  
A:Cross-references: UNIPROT:P07174; GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756  
R:Metzsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoic  
A:Reference number: PHI229; MUID:93077038; PMID:1448821  
A:Accession: PHI229  
A:Molecule type: DNA  
A:Residues: 1-20 <MET>  
A:Cross-references: GB:X61269  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C:Comment: This protein is thought to form a high-affinity receptor when it associates w  
C:Genetics:  
A:Introns: 20/3  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-425/Product: nerve growth factor receptor #status predicted <EXT>  
F:30-251/Domain: extracellular #status predicted <EXT>  
F:33-66/Domain: NGF receptor repeat homology <NG1>  
F:68-109/Domain: NGF receptor repeat homology <NG2>  
F:110-148/Domain: NGF receptor repeat homology <NG3>  
F:150-190/Domain: NGF receptor repeat homology <NG4>  
F:198-249/Region: serine/threonine-rich



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 74.1412 Seconds  
(without alignments)  
2769.633 Million cell updates/sec

Title: US-09-389-782a-2

Perfect score: 2179

Sequence: 1 MNKWLCCALLVLLDIIEWTT.....QKLFLEMIGNQVQSVKISCL 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	2179	100.0	401	1 T11B_MOUSE	O08712 mus musculus
2	2159	99.1	401	2 Q6P112	Q6P112 mus musculus
3	2079	95.4	401	1 T11B_RAT	O08727 rattus norv
4	1900	87.2	401	1 T11B_HUMAN	O00300 homo sapien
5	1014	46.5	387	2 Q6GLN3	Q6GLN3 xenopus lae
6	541	24.8	146	2 Q7Z2V4	Q7Z2V4 gallus gall
7	428	19.6	186	2 Q7Z2V5	Q7Z2V5 gallus gall
8	424.5	19.5	300	1 TR6B_HUMAN	Q95407 homo sapien
9	397.5	18.2	286	2 Q6NM61	Q6NM61 brachydanio
10	390.5	17.9	302	2 Q9PUS0	Q9PUS0 salvelinus
11	390	17.9	285	2 Q90W71	Q90W71 oncorhynch
12	383	17.6	285	2 Q90Y86	Q90Y86 oncorhynch
13	314	14.4	459	2 Q6Z327	Q6Z327 mus musculus
14	312	14.3	461	1 TR1B_HUMAN	P20333 h tumor nec
15	312	14.3	474	1 TR1B_MOUSE	P25119 mus musculus
16	301.5	13.8	655	1 TR21_HUMAN	Q75509 homo sapien
17	301	13.8	461	2 Q6VAU8	Q6VAU8 rattus norv
18	301	13.8	474	1 TR1B_RAT	Q80WY6 rattus norv
19	300.5	13.8	651	2 Q98SM6	Q98SM6 gallus gall
20	288	13.2	655	1 TR21_MOUSE	Q98PUS mus musculus
21	281	12.9	433	2 Q91ZM6	Q91ZM6 rattus norv
22	270	12.4	289	1 TNR5_MOUSE	P27512 mus musculus
23	270	12.4	289	1 Q8K2X6	Q8K2X6 mus musculus
24	268.5	12.3	467	2 Q80U10	Q80U10 gallus gall
25	268.5	12.3	625	1 TR11_MOUSE	Q35305 mus musculus
26	266.5	12.2	616	1 TR11_HUMAN	Q9Y6G6 homo sapien
27	266	12.2	462	2 Q80S50	Q80S50 gallus gall
28	263	12.1	457	2 Q81VS6	Q81VS6 homo sapien
29	263	12.1	483	2 Q800K7	Q800K7 paralyticthy
30	261	12.0	223	2 Q86YK5	Q86YK5 homo sapien
31	261	12.0	277	1 TNR5_HUMAN	P25942 homo sapien

32	254.5	11.7	318	2	Q7T2H3	Q7T2H3 oncorhynch
33	249	11.4	169	2	Q9JKE0	Q9JKE0 rattus norv
34	248	11.4	276	2	Q9DDD2	Q9DDD2 gallus gall
35	247.5	11.4	275	2	Q80WM9	Q80WM9 mus musculus
36	247.5	11.4	276	2	Q71F55	Q71F55 mus musculus
37	244	11.2	435	1	TNR3_HUMAN	P36941 homo sapien
38	243	11.2	278	2	Q8SQJ4	Q8SQJ4 sus scrofa
39	235	10.8	274	2	Q7YRL5	Q7YRL5 canis famlil
40	233.5	10.7	325	1	VT2_SFVKA	P25943 shope fibro
41	233.5	10.7	325	2	Q77FB3	Q77FB3 rabbit fibr
42	229	10.5	277	2	Q8WMO2	Q8WMO2 ovis aries
43	228	10.5	269	1	TNR5_BOVIN	Q28203 bos taurus
44	226	10.4	355	2	Q85308	Q85308 cowpox viru
45	224	10.3	349	2	O57098	O57098 camelpox vi

#### ALIGNMENTS

#### RESULT 1

ID	T11B_MOUSE	STANDARD;	PRT;	401 AA.
AC	O08712; O70202;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 11B precursor (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).			
DE	Name=Tnftrsf1b; Synonyms=OCIF, OPG;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C; TISSUE=Kidney;			
RX	MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;			
RA	Luethy R., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,			
RA	Simonet W.S., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,			
RA	Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,			
RA	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,			
RA	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,			
RA	Suggs S., Boyle W.J.;			
RT	"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";			
RL	Cell 89:309-319(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288 AND ARG-296.			
RC	STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;			
RX	MEDLINE=98382527; PubMed=9714833; DOI=10.1016/S0378-1119(98)00295-9;			
RA	Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,			
RA	Higashio K.;			
RT	"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";			
RL	Gene 215:339-343(1998).			
RN	[3]			
RP	FUNCTION.			
RX	MEDLINE=21060987; PubMed=10952716;			
RA	Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,			
RA	Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,			
RA	Simonet W.S.;			
RT	"Osteoprotegerin reverses osteoporosis by inhibiting endosteal osteoclasts and prevents vascular calcification by blocking a process resembling osteoclastogenesis.";			
RL	J. Exp. Med. 192:463-474(2000).			
CC	-!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.			

CC -I- SUBUNIT: Homodimer.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,  
 CC intestines and calvaria. Highly expressed in decidua and placenta,  
 CC and in embryo.  
 CC -I- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,  
 CC whereas expression decreases at day 11 and increases from day 15  
 CC to 17. On day 15 found in developing bone primordia,  
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,  
 CC abdominal aorta and midgut.  
 CC -I- INDUCTION: Up-regulated by TGF-beta and estrogens. Down-regulated  
 CC by 1,25-dihydroxyvitamin D3 and parathyroid hormone.  
 CC -I- SIMILARITY: Contains 2 death domains.  
 CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U94331; AAB33708.1; -;  
 DR EMBL; AB013898; BAA28269.1; -;  
 DR EMBL; AB013903; BAA33388.1; -;  
 DR EMBL; AB013899; BAA33388.1; JOINED.  
 DR EMBL; AB013900; BAA33388.1; JOINED.  
 DR EMBL; AB013901; BAA33388.1; JOINED.  
 DR EMBL; AB013902; BAA33388.1; JOINED.  
 DR HSSP; 014763; 1D0G.  
 DR MGD; MGI:109587; Tnfrsf11b.  
 DR GO; GO:0005578; C:extracellular matrix; IDA.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH like.  
 DR InterPro; IPR009030; Grow\_fac\_recept.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00017; DEATH DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 KW Apoptosis; Glycoprotein; Polymorphism; Receptor; Repeat; Signal.  
 FT SIGNAL 1 21 By similarity.  
 FT CHAIN 22 401 Tumor necrosis factor receptor  
 FT superfamily member 11b.  
 FT REPEAT 24 62 TNFR-Cys 1.  
 FT REPEAT 65 105 TNFR-Cys 2.  
 FT REPEAT 107 142 TNFR-Cys 3.  
 FT REPEAT 145 185 TNFR-Cys 4.  
 FT DOMAIN 198 269 Death 1.  
 FT DOMAIN 283 365 Death 2.  
 FT SITE 400 400 Involved in dimerization (By similarity).  
 FT DISULFID 41 54 By similarity.  
 FT DISULFID 44 62 By similarity.  
 FT DISULFID 65 80 By similarity.  
 FT DISULFID 83 97 By similarity.  
 FT DISULFID 87 105 By similarity.  
 FT DISULFID 107 118 By similarity.  
 FT DISULFID 124 142 By similarity.  
 FT DISULFID 145 160 By similarity.  
 FT DISULFID 166 185 By similarity.  
 FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).  
 FT VARIANT 138 138 R -> P (in strain 129/Ola and strain NIH  
 FT Swiss).  
 FT VARIANT 161 161 I -> R (in strain 129/Ola and strain NIH  
 FT Swiss).  
 FT VARIANT 165 165 N -> D (in strain 129/Ola and strain NIH  
 FT Swiss).

FT VARIANT 288 288 S -> A (in strain 129/Ola and strain NIH  
 FT Swiss).  
 FT VARIANT 296 296 L -> R (in strain 129/Ola and strain NIH  
 FT Swiss).  
 SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;  
 Query Match 100.0%; Score 2179; DB 1; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-143;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNKWLCCALLVLLDIIIEWTTQTETLPKYLHYDPETHGQLLCKCAPGTLYLKHQCTVRRKT 60  
 DB 1 MNKWLCCALLVLLDIIIEWTTQTETLPKYLHYDPETHGQLLCKCAPGTLYLKHQCTVRRKT 60  
 QY 61 LCVPCPDHSYDTSWHTSDECVYCSVCKELOSQVKECNRTHRVCECEGRVLETFCLK 120  
 DB 61 LCVPCPDHSYDTSWHTSDECVYCSVCKELOSQVKECNRTHRVCECEGRVLETFCLK 120  
 QY 121 HRSCTPGSGVVOAGTPERNTVCKKCPDGFSGTSSKAPCIKHTKNCSTFGLLLIQKGNAT 180  
 DB 121 HRSCTPGSGVVOAGTPERNTVCKKCPDGFSGTSSKAPCIKHTKNCSTFGLLLIQKGNAT 180  
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIPNWLSDVSLPOTKYNASVERI 240  
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFPRFAVPTKIIPNWLSDVSLPOTKYNASVERI 240  
 QY 241 KRRHSSQSQTFOLLKWKHQRNDQEMVKKIQDIDLCSSVORHLGHSNLTTEQLLALME 300  
 DB 241 KRRHSSQSQTFOLLKWKHQRNDQEMVKKIQDIDLCSSVORHLGHSNLTTEQLLALME 300  
 QY 301 SLPGKKISPEERTRTKTSKSEQLKLLSLWRINKNGQDTLKLGLMYALKHLKTSHPFKT 360  
 DB 301 SLPGKKISPEERTRTKTSKSEQLKLLSLWRINKNGQDTLKLGLMYALKHLKTSHPFKT 360  
 QY 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
 DB 361 VTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
 RESULT 2  
 Q6P112 PRELIMINARY; PRT; 401 AA.  
 AC Q6P112;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily, member 11b  
 DE (Osteoprotegerin).  
 GN Name=Thrsf11b;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=Limb;  
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP SEQUENCE FROM N.A.  
 RC Strausberg R.;  
 RD Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RE EMBL; BC049782; AAH49782.1;  
 RF GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.  
 RG GO: GO:0005615; C:extracellular space; TAS.  
 RH GO: GO:0042489; P:negative regulation of ontogenesis (sensu. . . ; IDA.  
 RI InterPro; IPR000488; Death.  
 RJ InterPro; IPR011029; DEATH like.  
 RK Pfam; PF00020; TNFR\_C6; 2.  
 RL SMART; SM00005; DEATH; 1.  
 RM SMART; SM00208; TNFR; 4.  
 RN PROSITE; PS00017; DEATH DOMAIN; 1.  
 RO PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 RP PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 RQ Receptor.  
 SQ SEQUENCE 401 AA; 45965 MW; 7C708E52EB46BA0E CRC64;  
  
 Query Match 99.1%; Score 2159; DB 2; Length 401;  
 Best Local Similarity 99.0%; Pred. No. 4.5e-142;  
 Matches 397; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 1 MNKWLCCALVLDIETWTTQETLPKYLHYDPETGHLCDKCAPGTLYKQHCIVRRKT 60  
 DB 1 MNKWLCCALVLDIETWTTQETLPKYLHYDPETGHLCDKCAPGTLYKQHCIVRRKT 60  
  
 QY 61 LCVPCPDHSYTDWHTSDVCYSPVKELQSVKQECNRTHNRVCEEGRYLEIFCLK 120  
 DB 61 LCVPCPDHSYTDWHTSDVCYSPVKELQSVKQECNRTHNRVCEEGRYLEIFCLK 120  
  
 QY 121 HRSPPGSGVQAGTPEKNTVCKKPDGPFSGTSSKAPCIKHTNCSTFGLLIQKGNAT 180  
 DB 121 HRSPPGSGVQAGTPEKNTVCKKPDGPFSGTSSKAPCIKHTNCSTFGLLIQKGNAT 180  
  
 QY 181 HDNVCSGNREATKCGIDVTLCBAPFPAVPTKIIPNWLVLVDSLPGTKVAESVERI 240  
 DB 181 HDNVCSGNREATKCGIDVTLCBAPFPAVPTKIIPNWLVLVDSLPGTKVAESVERI 240  
  
 QY 241 KRRHSSQEQTFOLLKWKHQNRODMVKKIIQIDILCESSVQRLHGHNSLTTEQLALME 300  
 DB 241 KRRHSSQEQTFOLLKWKHQNRODMVKKIIQIDILCESSVQRLHGHNSLTTEQLALME 300  
  
 QY 301 SLPGKISPEIERTRTKTKSSBQLLKLSLWRIKNGDQDTLKGMLYALKHLSHPFKT 360  
 DB 301 SLPGKISPEIERTRTKTKSSBQLLKLSLWRIKNGDQDTLKGMLYALKHLSHPFKT 360  
  
 QY 361 VTHSLRKTWFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
 DB 361 VTHSLRKTWFLHSFTMYRLYQKLFLEMIGNOVQSVKISCL 401  
  
 RESULT 3  
 ID\_T11B\_RAT STANDARD; PRT; 401 AA.  
 AC O08727;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 11B precursor  
 GN (Osteoprotegerin).  
 DE Names=tnfrsf11b; Synonyms=Ogp;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]

SEQUENCE FROM N.A.  
 TISSUE=Embryonic intestine;  
 MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;  
 Liemthuis W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,  
 Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 Suggs S., Boyle W.J.;  
 "Osteoprotegerin: a novel secreted protein involved in the regulation  
 of bone density";  
 Cell 89:309-319(1997).  
 -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes  
 its function in osteoclastogenesis. Inhibits the activation of  
 osteoclasts and promotes osteoclast apoptosis. Bone homeostasis  
 seems to depend on the local RANKL/OPG ratio. May also play a role  
 in preventing arterial calcification. May act as decoy receptor  
 for TRAIL and protect against apoptosis. TRAIL binding blocks the  
 inhibition of osteoclastogenesis (By similarity).  
 -!- SUBUNIT: Homodimer (By similarity).  
 -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 -!- INDUCTION: Up-regulated by osteopontin.  
 -!- SIMILARITY: Contains 2 death domains.  
 -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 -----  
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 or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
 -----  
 EMBL; U94330; AAB53707.1; -  
 HSSP; P19438; INCF.  
 RGD; 619802; Tnfrsf11b.  
 InterPro; IPR000488; Death.  
 InterPro; IPR011029; DEATH like.  
 InterPro; IPR009030; Growth factor receptor.  
 InterPro; IPR001368; TNFR\_C6.  
 Pfam; PF00020; TNFR\_C6; 4.  
 SMART; SM00005; DEATH; 1.  
 SMART; SM00208; TNFR; 4.  
 PROSITE; PS00017; DEATH DOMAIN; FALSE\_NEG.  
 PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 Apoptosis; Cytokine; Glycoprotein; Repeat; Signal.  
 SIGNAL 1 21 By similarity. Tumor necrosis factor receptor  
 CHAIN 22 401 superfamily member 11B.  
 REPEAT 24 62  
 REPEAT 65 105 TNFR-Cys 1.  
 REPEAT 107 142 TNFR-Cys 2.  
 REPEAT 145 185 TNFR-Cys 3.  
 REPEAT 198 269 TNFR-Cys 4.  
 DOMAIN 270 365 Death 1.  
 SITE 400 400 Death 2.  
 FT SITE 41 54 Involved in dimerization (By similarity).  
 FT DISULFID 44 62 By similarity.  
 FT DISULFID 65 80 By similarity.  
 FT DISULFID 83 97 By similarity.  
 FT DISULFID 87 105 By similarity.  
 FT DISULFID 107 118 By similarity.  
 FT DISULFID 124 142 By similarity.  
 FT DISULFID 145 160 By similarity.  
 FT DISULFID 166 185 By similarity.  
 FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 401 AA; 46192 MW; FECA31F1DAE573A CRC64;  
  
 Query Match 95.4%; Score 2079; DB 1; Length 401;

Best Local Similarity 94.5%; Pred. No. 1.6e-136;

Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKWLCCALLVLLDIIETWTQETLPKYLHYDPETGQHLCDKCAPTYLKHQCTVRRKT 60  
DB 1 MNKWLCCALLVLLDIIETWTQETFPKYLHYDPETGQHLCDKCAPTYLKHQCTVRRKT 60  
QY 61 LCVPCPDHSTWHTSDCVYCSVKELQSVKQECNTRNVRVCEBGRYLEIFCLK 120  
DB 61 LCVPCPDHSTWHTSDCVYCSVKELQSVKQECNTRNVRVCEBGRYLEIFCLK 120  
QY 121 HRSPPGSGVQAGTERTNVTCKKCPDGFSGTSSKAPCIKHTNCSTGILLIQGNAT 180  
DB 121 HRSPPGSGVQAGTERTNVTCKKCPDGFSGTSSKAPCIKHTNCSTGILLIQGNAT 180  
QY 181 HDNVCSGNEATQCCGIDVTLCEAEFFAVPTKIIPNWLVLVSLPCTKYNASVERI 240  
DB 181 HDNVCSGNEATQCCGIDVTLCEAEFFAVPTKIIPNWLVLVSLPCTKYNASVERI 240  
QY 241 KRRHSQEQTPQLKLWKHONRDQEMVKKIIQDIDLCSSVQRHGLSHNLTTQQLALME 300  
DB 241 KRRHSQEQTPQLKLWKHONRDQEMVKKIIQDIDLCSSVQRHGLSHNLTTQQLALME 300  
QY 301 SLPGKISPEERTFTKTSSEOLLKLSLWRKNGDQDTLKLGMVYALKHKTSHFPKT 360  
DB 301 SLPGKISPEERTFTKTSSEOLLKLSLWRKNGDQDTLKLGMVYALKHKTSHFPKT 360  
QY 361 VTHSLRKTWRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401  
DB 361 VTHSLRKTWRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401

## RESULT 4

T11B HUMAN STANDARD; PRT; 401 AA.  
AC 000300; 060236; Q9UHP4;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 11B precursor  
(Osteoprotegerin) (Osteoclastogenesis inhibitory factor).  
GN Names=TNFRSF11B; Synonyms=OCIF, OPG;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=97262071; PubMed=9108485; DOI=10.1016/S0092-8674(00)80209-3;  
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
RA Suggs S., Boyle W.J.;  
RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
RT of bone density";  
RL Cell 89:309-319(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung cancer;  
RX MEDLINE=98151033; PubMed=9492069; DOI=10.1210/en.139.3.1329;  
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
RA Tsuda E., Morinaga T., Higashio K.;  
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
RT osteoclastogenesis in vitro";  
RL Endocrinology 139:1329-1337(1998).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.  
RC TISSUE=Placenta;

RE MEDLINE=98351569; PubMed=9688283;  
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
RT "Cloning and characterization of the gene encoding human  
RT osteoprotegerin/osteoclastogenesis-inhibitory factor";  
RL Eur. J. Biochem. 254:685-691(1998).  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANTS ASN-3 AND MET-104.  
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,  
RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;  
RT "NIHNS-SNPs, environmental genome project, NIHNS ES15478, Department  
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)";  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP SEQUENCE OF 22-36 AND 378-401.  
RX MEDLINE=98238645; PubMed=9571159; DOI=10.1006/bbrc.1998.8443;  
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,  
RA Morinaga T., Tsuda E., Higashio K.;  
RT "Characterization of monomeric and homodimeric forms of  
RT osteoclastogenesis inhibitory factor";  
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).  
RN [7]  
RP SEQUENCE OF 22-36.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RL verified cleavage sites";  
RN Protein Sci. 13:2819-2824(2004).  
RN [8]  
RP SEQUENCE OF 22-393 FROM N.A.  
RC TISSUE=Placenta;  
RX PubMed=12110935;  
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;  
RT "Cloning and expression of osteoprotegerin from Homo sapiens";  
RL Acta Biochim. Biophys. Sin. 31:680-684(1999).  
RN [9]  
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION  
RX MEDLINE=97312536; PubMed=9168977; DOI=10.1006/bbrc.1997.6503;  
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,  
RA Morinaga T., Higashio K.;  
RT "Isolation of a novel cytokine from human fibroblasts that  
RT specifically inhibits osteoclastogenesis";  
RL Biochem. Biophys. Res. Commun. 234:137-142(1997).  
RN [10]  
RP TRAIL BINDING.  
RX MEDLINE=98269100; PubMed=9603945; DOI=10.1074/jbc.273.23.14363;  
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,  
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,  
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;

"Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";  
 [11]  
 RL J. Biol. Chem. 273:14363-14367(1998).  
 RN  
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.  
 RX MEDLINE=98148058; PubMed=9478964; DOI=10.1074/jbc.273.9.5117;  
 RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,  
 RA Morinaga T., Higashio K.;  
 RT "Characterization of structural domains of human osteoclastogenesis  
 RT Inhibitory factor.";  
 RL J. Biol. Chem. 273:5117-5123(1998).  
 RN  
 RP REVIEW.  
 RX MEDLINE=21395914; PubMed=11505389;  
 RX DOI=10.1002/1097-0142(20010801)32:3<460::AID-CNCR1344>3.0.CO;2-D;  
 RA Hofbauer L.C., Neubauer A., Heufelder A.E.;  
 RT "Receptor activator of nuclear factor-kappaB ligand and  
 RT osteoprotegerin: potential implications for the pathogenesis and  
 RT treatment of malignant bone diseases.";  
 RL Cancer 92:460-470(2001).  
 RN  
 RP VARIANT JPD ASP-182 DEL.  
 RX PubMed=12189164; DOI=10.1093/hmg/11.18.2119;  
 RA Cundy T., Hegde M., Naot D., Chong B., King A., Wallace R., Mulvey J.,  
 RA Love D.R., Seidel J., Fawcett M., Banovic T., Callon K.E., Grey A.B.,  
 RA Reid I.R., Middleton-Hardie C.A., Cornish J.;  
 RT "A mutation in the gene TNFRSF11B encoding osteoprotegerin causes an  
 RT idiopathic hyperphosphatasia phenotype.";  
 RL Hum. Mol. Genet. 11:2119-2127(2002).  
 CC  
 CC -I- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes  
 CC its function in osteoclastogenesis. Inhibits the activation of  
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone  
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also  
 CC play a role in preventing arterial calcification. May act as decoy  
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding  
 CC blocks the inhibition of osteoclastogenesis.  
 CC  
 CC -I- SUBUNIT: Homodimer.  
 CC  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC  
 CC -I- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,  
 CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,  
 CC lymph node, trachea, adrenal gland, testis, and bone marrow.  
 CC Detected at very low levels in brain, placenta and skeletal  
 CC muscle. Highly expressed in fetal kidney, liver and lung.  
 CC  
 CC -I- INDUCTION: Up-regulated by increasing calcium-concentration in the  
 CC medium and estrogens. Down-regulated by glucocorticoids.  
 CC  
 CC -I- PTM: N-glycosylated. Contains sialic acid residues.  
 CC  
 CC -I- PTM: The N-terminus is blocked.  
 CC  
 CC -I- DISEASE: Defects in TNFRSF11B are the cause of juvenile Paget  
 CC disease (JPD) [MIM:239000]; also called hyperostosis corticalis  
 CC deformans juvenilis or hereditary hyperphosphatasia or chronic  
 CC congenital idiopathic hyperphosphatasia. JPD is a rare autosomal  
 CC recessive osteopathy that presents in infancy or early childhood.  
 CC The disorder is characterized by rapidly remodeling woven bone,  
 CC osteopenia, debilitating fractures, and deformities due to a  
 CC markedly accelerated rate of bone remodeling throughout the  
 CC skeleton. Approximately 40 cases of JPD have been reported  
 CC worldwide. Unless it is treated with drugs that block osteoclast-  
 CC mediated skeletal resorption, the disease can be fatal.  
 CC  
 CC -I- SIMILARITY: Contains 2 death domains.  
 CC  
 CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL; U94332; AAB53709.1; -;  
 CC EMBL; AB021446; BAA25910.1; -;  
 CC EMBL; AB008822; BAA32076.1; -;  
 CC EMBL; AB008821; BAA32076.1; JOINED.  
 CC EMBL; AY466112; AAR23265.1; -;

DR EMBL; BC030155; AAB30155.1; -;  
 DR EMBL; AF134187; AAF20168.1; -;  
 DR HSSP; O14763; 1DOG.  
 DR Genew; HGNC:11909; TNFRSF11B.  
 DR H-InvDB; HIX0007748; -;  
 DR MIM; 603643; -;  
 DR MIM; 239000; -;  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0005125; F:cytokine activity; TAS.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR GO; GO:0001501; P:skeletal development; TAS.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; Death-like.  
 DR InterPro; IPR009030; Growth\_fac\_recept.  
 Query Match 87.2%; Score 1900; DB 1; Length 401;  
 Best Local Similarity 85.8%; Pred. No. 4.6e-124;  
 Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;  
 QY 1 MNKWLCCALLVLLDI-IEWTQTETPLPKYLHYDPETGHQLLCKCAPGTLYLKQHTVRRK 59  
 DB 1 MNKLLCCA-LVFLDISIKWTQTETPPKYLHYDEETSHQLLCKCPPTLYLKQHTAKWK 59  
 QY 60 TLICVPCDHSYDTSWHTSDECVYCSVCKELQSVKQECNRTHNRVCECEGRVLEIEFCL 119  
 DB 60 TVCAPCDHYTDSWHTSDECLYCSVPCKELQYVQECNRTHNRVCECEGRVLEIEFCL 119  
 QY 120 KHRSCPPGSGVQAGTPERTVCKCPDGGFFSGTSSKAPCIKHTNCSTFGLLLIOGNA 179  
 DB 120 KHRSCPPGSGVQAGTPERTVCKCPDGGFFSGTSSKAPCIKHTNCSTFGLLLIOGNA 179  
 QY 180 THDNVCSGNREATQKCGIDVTLCCEAFFRPAVPTKIIPNWLSDLPLGCTKVNESVER 239  
 DB 180 THDNVCSGNREATQKCGIDVTLCCEAFFRPAVPTKIIPNWLSDLPLGCTKVNESVER 239  
 QY 240 IKRHSQSQTFTOLLKWKHQRNDQWVKIIQDIDLCSSVORHLGHSNLTTEQLLALM 299  
 DB 240 IKRHSQSQTFTOLLKWKHQRNDQWVKIIQDIDLCSSVORHLGHSNLTTEQLLALM 299  
 QY 300 ESLPGKKISPEETERTKTKSSEQLLKLWLRIKNGDQDTLKLWYALVHLKHTSHFPK 359  
 DB 300 ESLPGKKISPEETERTKTKSSEQLLKLWLRIKNGDQDTLKLWYALVHLKHTSHFPK 359  
 QY 360 TVTHSLRKTMRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
 DB 360 TVTQSLKKTIRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL 401  
 RESULT 5  
 Q6GLN3 PRELIMINARY; PRT; 387 AA.  
 ID Q6GLN3  
 AC Q6GLN3  
 DT 05-JUL-2004 (TREMblrel. 27, Created)  
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
 DE MGC84670 protein.  
 GN Name=MGC84670;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA	Brownstein M.J., Uedlin T.B., Toshuyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA	Fahay J., Helton E., Katteman M., Madan A.C., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.W., Green E.D., Dickinson M.C.,
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA	Krzywinski A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Jones S.J., Marra M.A., Skaleka U., Smallick D.E., Schnerch A., Schein J.E.,
RA	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Eye;
RC	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
EX	Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.;
RA	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT	initiative.";
RT	Dev. Dyn. 225:384-391(2002).
RN	[3]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Eye;
RC	Klein S., Gerhard D.S.;
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC074428; AAH74428.1; -
DR	GO; GO:0004872; F-receptor activity; IEA.
DR	InterPro; IPR006209; EGF like.
DR	Pfam; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 2-
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS00452; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PSS0020; TNFR_NGFR_2; 2.
SQ	SEQUENCE 387 AA; 44568 MW; F365C364A11484AA CRC64;
Query Match            46.5%; Score 1014; DB 2; Length 387;	
Best Local Similarity   47.2%; Pred. No. 1.9e-62;	
Matches 188; Conservative 66; Mismatches 130; Indels 14; Gaps	
QY	1 MNKLCALLVLLDIIIEWTTOETLPKYHYDPETHQLLCDKCAPGYLKQHCTVRRKT
Db	: :
QY	1 MYRMISRTLVLHL-LSLAGNSVPVKYSHYDPTSMYLQCDHCPCGTYYKDCSTSEKNT
Db	: :
QY	61 LCVPCEHSIDTSWHTSDEVCYSPVCKELQSVCQNTRHNRVCEBEGRYLEIFCLK
Db	: :
QY	60 ECAPCPSHYNDRWNSENTECOFCNVCKELQYVQCNCNTHNLCECAAGFYLDLFCEPV
Db	: :
QY	121 HRSCPFGSVQVAGTPERTNKKCPDGFTSGESKAPCIKTNCSFTGLLLI QKGNAI
Db	: :
QY	120 HKKHCHPGVQAQGEPTSDTVCRCPGTFSDSTSATARCQKHCTCKGIGIVAYOGDS
Db	: :
QY	181 HDNVCNGREATQKGI DVTLCEAEFFRAFVPTKIIPNMLSLVDLSLPGTKVAESVERI
Db	: :
QY	180 HDTLCC--QPESFCEIDITLCQAEFFRF-VPN----NWLTATAQRPPSTWSSQIEGV
Db	: :
QY	241 KRHSSEQGTOLLKLWKHQNRDQMVKKI IQIDICCESSVRQHLGHSLNTEQILLALME
Db	: :
QY	232 QEKRDPOHAFLFKLWKDHNRSESGKHLFDQLQVCEKKVXKHGRLVNVTARLTLMK
Db	: :
QY	301 SLUPGGKISPEETERPKTKSSLOLLKLLSWIRLKGDDOOLKGLMYALKHLTKTSHPKT
Db	: :
QY	292 SLPGNKISKRELETTVKICROPDQVLLKNLRNKGNG-DTIN---LLKVTKTNRLQRM
Db	: :
QY	361 VPHSLRKTWRFILSHSTFWYRLYOKLFLWMIGNQVQSVKI 398
Db	: :
QY	347 LRRTIKLEQFLNSDEMWRLYOKLLLIIFGSQTQPAKV 384
Db	: :
RESULT 6	

DR GO: GO:0004872; F:receptor activity; IEA.  
 DR InterPro: IPR006209; EGF\_like.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS00052; TNFR\_NGFR\_2; 1.  
 KW Receptor.  
 FT NON TPR 186  
 SQ SEQUENCE 186 AA; 20671 MW; 31D65731DACB7508 CRC64;

Query Match 19.68; Score 428; DB 2; Length 186;  
 Best Local Similarity 47.98; Pred. No. 4.5e-22;  
 Matches 70; Conservative 23; Mismatches 53; Indels 0; Gaps 0;

QY 25 PPKYLHYDPETGHQLCDKCAPGYLKQKHTVRRKTLCPVCPDHSYTDSDWHTSDCVYCS 84  
 DB 32 PFTYQWRDAGTKERVTCQCPGTFVQAQHTKERTVCACPDLHYTHYNYLEKCLYCN 91  
 QY 85 PVCKELQSVQKQNRTHNRVCEEGRYLIEIFCLKHSRCPGSGVGVQAGTPTNRTVCKK 144  
 DB 92 VXCGERQVEVQCQCNATHNACQCEGPHAEWFCVQHXKXPGSGVGVKLGSPSENTQCR 151  
 QY 145 CPDGFSGSETSSKAPCIKHTNSTFG 170  
 DB 152 CPRGSFSSSSSTPECPRAHQNTQLG 177

## RESULT 8

TR6B\_HUMAN STANDARD; PRT; 300 AA.  
 AC 095407;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (Dcr3) (M68)  
 DE (UNQ186/PRO312)  
 GN Name=TNFRSF6B; Synonyms=Dcr3, TR6;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal lung;  
 RX MEDLINE=99087326; PubMed=9872321; DOI=10.1038/25387;  
 RA Patti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,  
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,  
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,  
 RA Goddard A.D., Botstein D., Ashkenazi A.;  
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer.";  
 RT Nature 396:699-703 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.  
 RC TISSUE=Prostate;  
 RX MEDLINE=99253915; PubMed=10318773; DOI=10.1074/jbc.274.20.13733;  
 RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
 RT "A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";  
 RL J. Biol. Chem. 274:13733-13736 (1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=20122600; PubMed=10655513; DOI=10.1073/pnas.97.3.1230;  
 RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,  
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;  
 RT "Overexpression of M68/Dcr3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235 (2000).  
 RL

RA [4]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens J.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Smith J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
 RT Genome Res. 13:2265-2270 (2003).  
 RL  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RX Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A.G., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharvalho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sultson J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RT Nature 414:865-871 (2001).  
 RL  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Lung, and Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT and TNFSF6/FASL. Protects against apoptosis.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.  
CC detected in adult stomach, spinal cord, lymph node, trachea,  
CC spleen, colon and lung. Highly expressed in several primary tumors  
CC from colon, stomach, rectum, esophagus and in SW480 colon  
CC carcinoma cells.  
CC  
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC  
CC -----  
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC ENBL; AF104419; AAD03056.1; -  
CC ENBL; AF134240; AAD29688.1; -  
CC ENBL; AF217796; AAF35244.1; -  
CC ENBL; AF217793; AAF33685.1; -  
CC ENBL; AF217794; AAF33686.1; -  
CC ENBL; AY358279; AAQ88646.1; -  
CC ENBL; AL121845; CAC03668.1; -  
CC ENBL; BC017065; AAH17065.1; -  
CC ENBL; BC034349; AAH34349.1; -  
CC HSP; O14763; IDU3.  
CC Genew; HGNC:11921; TNFRSP6B.  
CC H-InVDB; HIX0016007; -  
CC MIM; 603361; -  
CC GO; GO:0005625; C:soluble fraction; TAS.  
CC GO; GO:0004872; F:receptor activity; TAS.  
CC GO; GO:0006916; P:anti-apoptosis; TAS.  
CC InterPro; IPR009030; G:row fac\_recept.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00020; TNFR\_c6; 4.  
CC SMART; SM00208; TNFR\_4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
CC PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
CC Apoptosis; Direct protein sequencing; Glycoprotein; Receptor; Repeat;  
KW SIGNAL.  
FT SIGNAL 1 29  
FT CHAIN 30 300 Tumor necrosis factor receptor  
FT  
FT superfamily member 6B.  
FT REPEAT 31 70  
FT REPEAT 72 113 TNFR-Cys 1.  
FT REPEAT 115 150 TNFR-Cys 2.  
FT REPEAT 152 193 TNFR-Cys 3.  
FT REPEAT 196 239 TNFR-Cys 4.  
FT DISULFID 49 62 By similarity.  
FT DISULFID 52 70 By similarity.  
FT DISULFID 73 88 By similarity.  
FT DISULFID 91 105 By similarity.  
FT DISULFID 95 113 By similarity.  
FT DISULFID 115 126 By similarity.  
FT DISULFID 132 150 By similarity.  
FT DISULFID 153 168 By similarity.  
FT DISULFID 174 193 By similarity.  
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;  
Query Match 19.5%; Score 424.5; DB 1; Length 300;  
Best Local Similarity 39.0%; Pred. No. 1.4e-21;  
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;  
QY 26 PKYLHDPETGHLCDKCAPGYLKHQCTVRRKTLVCPDHSYTDSDHMTSDECVCSVC 85  
DB 34 PTYPWRDAETGRVLCAQCPGPTGVRPCRRSDPTTCGPPRHVTQFWNYLCRYCNV 93  
QY 86 VKELQSVKQECNRTNVRVCEEGRYLEIFCLKHSRCPGSGVQVQAGTPERTVCKK 145  
DB 94 LCGEEREEARACHATHNRACRRTGFFAHAGFLEHASCPPGAGVIAFGTPTSQNTQCPC 153  
QY 146 PDGFFSGTSSKAPCIKHTNCTGFLGILTIQKNATHDNV---CSGNREATORCGIDVTLC 202  
DB 154 PGTFSASSSSSEQCPHNCNTALGALNVPSSSHDTLCTSGTFFPLSTRVPGAE--C 211

QY 203 EEAFFRAVPTTKIIPNWLVLVDSL 227  
DB 212 ERAVIDFAVQDISIKRLQRLQAL 236

## RESULT 9

Q6NW61 PRELIMINARY; PRT; 286 AA.  
AC Q6NW61;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE LOC007674 protein (Fragment).  
GN Name=LOC007674;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Strausberg R.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC067712; AAH67712.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR\_4.  
DR PROSITE; PS01186; EGF 2; UNKNOWN 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN 1.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
FT NON TER 1  
SQ SEQUENCE 286 AA; 32275 MW; 9F43CDC5FAC4E77B CRC64;  
Query Match 18.2%; Score 397.5; DB 2; Length 286;  
Best Local Similarity 31.6%; Pred. No. 9.8e-20;  
Matches 94; Conservative 44; Mismatches 118; Indels 41; Gaps 6;  
QY 28 YLHVDPEHGHLCDKCAPGYLKHQCTVRRKTLVCPDHSYTDSDHMTSDECVCSVC 87  
DB 18 YRRKDPETGRTLECARCAPGSRRLQHCSSSRQTCSPGPGMYTFWNYIPDCLLDS-C 76  
QY 88 KELOSQVQECNRTNVRVCEEGRYLEIFCLKHSRCPGSGVQVQAGTPERTVCKKCPD 147  
DB 77 AHRVVQPCNGIANTVCECEEGFYWQHFCRRHSVCRPGHGVKTAGTFFYSYDTCVCAEC 136

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QY 148 GPFSGTSSKAPCIKHTNCTGFLLLIQKNATHNVCSGNREARATQKCGIDVTLCEAFF 207
DB 137 GHFSDATKAQAQVHRVCGEHEHLL--SGNTHYNSICTTCQQLSNGTWTVAVFPAL 195
QY 208 RPAVPTKIPIWLSVLVDSLPGTKVAESVERIKRRHSQEQTFQLLKLWKHQNRQEMV 267
DB 196 ALQVQKIDIRLEQWV-----IRRLKK-----PLKQLHK----- 225
QY 268 KKIIDIDLCSSVQRHLGHSNITTTQLLALMSLPFKKISPRIERTKTKSSQ 324
DB 226 RTAMRRADPSEGLDRSMLENSYLHSLAQM-----TQNIIRVQSCNNIER 273

RESULT 10
Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz P.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation.";
RL Biol. Reprod. 62:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; IDAV.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 17.9%; Score 390.5; DB 2; Length 302;
Best Local Similarity 42.7%; Pred. No. 3.2e-19;
Matches 67; Conservative 34; Mismatches 53; Indels 3; Gaps 2;

QY 32 DPETGQLLDCAPGTYLKQHTVVRKTLVCPDPHSYTDSDWHTSDECVYCSVPCKELQ 91
DB 27 DRYSGLSIVCDRCPGGTYLRAPGSARWKSQDCAPNGAYTEFWNHLSKCLRCS--MCAENQ 85

QY 92 SVKQECNRTHRVCEBGRYL--EIEFLKHSRCPGSGVGVQAGTPERNVCKPDGF 149
DB 86 VVQECSPSNCECEKGEYFNKVEACIKHKECPGCGANTGTGPHQDTECVQCAQGF 145

QY 150 PSGETSKAPCIKHTNCTGFLLLIQKNATHNVCS 186
DB 146 YSEVSSAKATCLAQSNCKVGGLRWLKGQDWHNTLCA 182

RESULT 11
Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Pleguezuelos O., Secombes C.J.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ315137; CAC43329.1; -.
DR HSSP; O14763; IDOG.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31642 MW; FB75CFFC1B391AD0 CRC64;

Query Match 17.9%; Score 390; DB 2; Length 285;
Best Local Similarity 40.5%; Pred. No. 3.3e-19;
Matches 79; Conservative 25; Mismatches 81; Indels 10; Gaps 4;

QY 26 PKYLHYDPETGQLLDCAPGTYLKQHTVVRKTLVCPDPHSYTDSDWHTSDECVYCS 85
DB 29 PTYIWRDDATGDSLTCDLCAPGTYLKQHTVVRKTLVCPDPHSYTDSDWHTSDECVY 88

QY 86 VC--KELOSVQKQECNRTHRVCEBGRYLETEFLKHSRCPGSGVGVQAGTPERNVCK 143
DB 89 FCTADEIESV--PCTQLHNRQCECKDGFYTHGSCSRHRRCPPGEGVINGTAHTDVKE 146

QY 144 KCPDGFSGTSSKAPCIKHTNCTGFLLLIQKNATHNVCS----GNREATQKCGIDV 199
DB 147 PCPVGFFSAVSSSRKACQKFSVCPGGTTI--PGNDMDNVYCSACTNGSRTHEGAICDG 204

QY 200 TLCEAFAFPFAVPTK 214
DB 205 ELMEFLSLQLTPRK 219

RESULT 12
Q90YS6 PRELIMINARY; PRT; 285 AA.
AC Q90YS6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TNF decoy receptor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21883732; PubMed=11886174; DOI=10.1006/cyto.2001.0979;
RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT fragments containing AU-rich elements.";
RL Cytokine 17:71-81(2002).
DR EMBL; AF401631; AAK91758.1; -.
DR HSSP; O14763; IDOG.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31795 MW; 5E3BD1B6EFC6BABC CRC64;

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Query Match 17.6%; Score 383; DB 2; Length 285;
Best Local Similarity 41.0%; Pred. No. 1e-18;
Matches 80; Conservative 24; Mismatches 81; Indels 10; Gaps 5;

QY 26 PKYLHYDPETHGOLLCDKCAPGYLKQHCTVRKTLVCPDHSYTDSTWHTSDECVYCS 85
DB 29 PTYIWRDDATGDSLTCDLCAAGYLLKHCTKDRKSDGCPKSHYTEIWNRYCQYCN 88
QY 86 VC--KELQSVKQECNRTHNRVCEBGRYLEIEFCLKHSRCPGSGVVOAGTPERNVT 143
DB 89 FCTADIESV--FCTQLHNRQCECKDGFYTHGSCSRHRCPGEGVINGTAHTDVKE 146
QY 144 KCPDGFSGTSSKAPCIKHTNGSTFGLLLIQKNATHDNVCS---GNREATQKCGIDV 199
DB 147 PCFVGFFSAVSSSRKACQKFSVCP-GRVTI-PGNDMNDVYCSACRNGSKRTHGQAIC 204
QY 200 TLCCEAFFRFAVPTK 214
DB 205 ELMEFLSLQLLTLPK 219

RESULT 13
Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DE Tumor necrosis factor receptor 2 (TNFR2) (Last sequence update)
DE Tumor necrosis factor receptor 2 protein (Fragment).
GN Name=TNFRsf1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR F019; 148854; 148854.
DR HSSP; P19438; 1NCF.
DR MGD; MGI:1314983; Tnfrsf1b.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0018021; C:integral to membrane; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008220; P:necrosis; IMP.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER
FT SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 14.4%; Score 314; DB 2; Length 459;
Best Local Similarity 34.6%; Pred. No. 1.1e-13;
Matches 66; Conservative 20; Mismatches 79; Indels 26; Gaps 4;

QY 18 WTTQETLPPKYL--HYDPETHG-----QLLCDKCAPGYLKQHCTVRKTL 62
DB 2 WATCTVPAQVVLTPYKDPGVECCISQSYDRKQAMCCAKCPGQYVHFCNKTSDTVC 61
QY 63 VPCPHSYTDSWHTSDECVYCSFVKELQSVKQECNRTHNRVCEBGRYLEIEF----- 117
DB 62 ADCEASMTYQVWNQFRITCLSSSSSCSTQVETRACTQQNRVCAACEAGRYCALKTHSG 121
QY 118 --CLHRSRCPGSGVVOAGTPERNVTCKPCPDGFFSGETSSKAPCIKHTNCSTFGLLL 175
DB 122 RQCMRLSKGPGFGVASSRAPNGNLKACAPGTFTSDTSSDVRPHRICS-----ILAI 177
QY 176 KGNATHDNVCS 186
DB 178 PGNASTDAVCA 188

RESULT 14
TRIB HUMAN
ID TRIB HUMAN STANDARD; PRT; 461 AA.
AC P20333; Q16042; O6Y129; Q9UIH1;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor
DE type II) (p75) (p80 TNF-alpha receptor) (CD120b) (Stanacept)
DE [Contains: Tumor necrosis factor binding protein 2 (TBP2) (TBP-2)].
GN Name=TNFRSF1B; Synonyms=TNFR, TNFR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-196.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=96299745; PubMed=8661109; DOI=10.1006/geno.1996.0327;
RA Beltlinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND FUNCTION OF
RP ISOFORM 2
RX PubMed=14688072; DOI=10.1093/intimm/dxh014;
RA Lainez B., Fernandez-Real J.M., Romero X., Esplugues E., Canete J.D.,
RA Ricart W., Engel P.;
RT "Identification and characterization of a novel spliced variant that
RT encodes human soluble tumor necrosis factor receptor 2.";
RL Int. Immunol. 16:169-177(2004).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS MET-187; ARG-196; LYS-232; THR-236;
RP PRO-264 AND ARG-295.
RA Rieder M.J., Livingston R.J., Daniele M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIHES-SNP8, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
```

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND  
RP ARG-301.  
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,  
RA Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,  
RA Nickerson D.A.;  
RA "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-  
RT PHRCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RP TISSUE=PNS;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8]  
RP SEQUENCE OF 37-461 FROM N.A. (ISOFORM 1).  
RX MEDLINE=91370690; PubMed=1965549; DOI=10.1016/1043-4666(90)90022-I;  
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,  
RA Brockhaus M., Lesslauer W.;  
RT "Two human TNF receptors have similar extracellular, but distinct  
RT intracellular, domain sequences.";  
RL Cytokine 2:231-237(1990).  
RN [9]  
RP SEQUENCE OF 116-461 FROM N.A. (ISOFORM 1), PARTIAL SEQUENCE, AND  
RP VARIANT ARG-196.  
RX MEDLINE=90349572; PubMed=2166946;  
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
RA Ringold G.M.;  
RT "Complementary DNA cloning of a receptor for tumor necrosis factor and  
RT demonstration of a shed form of the receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
RN [10]  
RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21069356; PubMed=11197692; DOI=10.1038/sj.gene.6363700;  
RA Teuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;  
RT "New single nucleotide polymorphisms in the coding region of human  
RT TNFR2: association with systemic lupus erythematosus.";  
RL Genes Immun. 1:501-503(2000).  
RN [11]  
RP SEQUENCE OF 27-31.  
RC TISSUE=Urine;  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human urine.  
RT Evidence for immunological cross-reactivity with cell surface tumor  
RT necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [12]  
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
RX MEDLINE=91056048; PubMed=2173696;  
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
RA Brockhaus M.;  
RT "Purification and partial amino acid sequence analysis of two distinct

RT tumor necrosis factor receptors from HL60 cells.";  
RL J. Biol. Chem. 265:20131-20138(1990).  
RN [13]  
RP CHARACTERIZATION.  
RX MEDLINE=93016040; PubMed=1328224;  
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
RA Lipari M.T., Goeddel D.V.;  
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
RT Characterization of ligand binding, internalization, and receptor  
RT phosphorylation.";  
RL J. Biol. Chem. 267:21172-21178(1992).  
RN [14]  
RP INTERACTION WITH TRAF2.  
RX MEDLINE=94349371; PubMed=8059916; DOI=10.1016/0092-8674(94)90532-0;  
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;  
RT "A novel family of putative signal transducers associated with the  
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";  
RL Cell 78:681-692(1994).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
RP TRAF2.  
RX MEDLINE=99221490; PubMed=10206649; DOI=10.1038/19110;  
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
RT "Structural basis for self-association and receptor recognition of  
RT human TRAF2.";  
RL Nature 398:533-538(1999).  
RN [16]  
RP VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21603988; PubMed=11762942;  
RA Morita C., Horiuchi T., Tsukamoto H., Hattori N., Kikuchi Y.,  
RA Arinobu Y., Otsuka T., Sawabe T., Harashina S., Nagasawa K., Niho Y.;  
RT "Association of tumor necrosis factor receptor type II polymorphism  
RT 196R with systemic lupus erythematosus in the Japanese: molecular and  
RT functional analysis.";  
RL Arthritis Rheum. 44:2819-2827(2001).  
RN [17]  
RP VARIANT ARG-196.  
RX MEDLINE=22151311; PubMed=12161545; DOI=10.1210/jc.87.8.3977;  
RA Peral B., San Millan J.L., Castello R., Moghetti P.,  
RA Escobar-Morreale H.F.;  
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the  
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic ovary  
RT syndrome and hyperandrogenism.";  
RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).  
RN [18]  
RP FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and  
RP approximately 5-fold lower affinity for homotrimeric  
RP TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the  
RP apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. This  
RP receptor mediates most of the metabolic effects of TNF-alpha.  
RP Isoform 2 blocks TNF-alpha-induced apoptosis, which suggests that  
RP it regulates TNF-alpha function by antagonizing its biological  
RP activity.  
RN [19]  
RP SUBUNIT: Binds to TRAF2.  
RP SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);  
RP secreted (isoform 2 and TRP-II).  
RN [20]  
RP ALTERNATIVE PRODUCTS:  
RP Event=Alternative splicing; Named isoforms=2;  
RP Name=1;  
RP IsoId=P20333-1; Sequence=Displayed;  
RP Name=2; Synonyms=DS-TNFR2(Delta57.8), sTNFR2;  
RP IsoId=P20333-2; Sequence=VSP\_011826, VSP\_011827;  
RP PTM: Phosphorylated; mainly on serine residues and with a very low  
RP level on threonine residues.  
RP PTM: A soluble form (tumor necrosis factor binding protein 2) is  
RP produced from the membrane form by proteolytic processing.  
RP PHARMACEUTICAL: Available under the name Enbrel (Immunex and  
RP Wyeth-Ayerst). Used to treat moderate to severe rheumatoid  
RP arthritis (RA). Enbrel consist of the extracellular ligand-binding  
RP portion of TNFRSF1B linked to an immunoglobulin Fc chain. It binds  
RP to TNF-alpha and blocks its interactions with receptors.  
RN [21]  
RP SIMILARITY: Contains 4 TNFR-Cys repeats.  
RN [22]  
RP DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;

Query Match 14.3%; Score 312; DB 1; Length 461;  
 Best Local Similarity 34.7%; Pred. No. 1.5e-13;  
 Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALAVLLDIIEWTQTETLPK--YLHYDPEYCH-----QLLCKKCAPGTYLKQH 53  
 DB 9 ALAVGLLEL--WAAAHALFAQVATTPYAPGPGTCLRLREYYDQTAQCMCCSKSPGQAKVF 66  
 QY 54 CTVRRRTLCVPCPDHSDYTSWHTSDCVYSPVKELQSVKQRCNTHNRVCEBGRYL 113  
 DB 67 CTYKTSVTCVDCSDSYTYQLNWWPECLSGCRSSDQVETQACTREONRICTCRPGWYC 126  
 QY 114 EI-----EFLKHSRCPGSGVQAGTPERNVTKKCPDGFSGTSSKAPCIKHTNCS 167  
 DB 127 ALSQKQGCRLCAPLRCRPGFVGARPGTETSDVVKPCAPGTSTNTSSDTCRPHQICN 186  
 QY 168 TFGLLLIQKNATHDNVCS 186  
 DB 187 VWAI-----PGNASMDAVCT 201

## RESULT 15

TRIB MOUSE  
 ID TR1B MOUSE STANDARD; PRT; 474 AA.  
 AC P25119; O88734; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DE 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor  
 DE necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor  
 DE type II) (p75) (p80 TNF-alpha receptor).  
 GN Name:tnfrsf1b; Synonyms:tnfr-2, Tnfr2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=91187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H.,  
 RA Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=98414512; PubMed=9740674; DOI=10.1006/geno.1998.5407;  
 RA Hurlie B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;  
 RT "The mouse tumor necrosis factor receptor 2 gene: genomic structure  
 RT and characterization of the two transcripts.";  
 RL Genomics 52:79-98(1998).  
 RN [4]  
 SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN=NOD;  
 RA Jacob C.O., Liu J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RA Kisonerghis M., Fellores R., Feldmann M., Chernajovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and  
 CC approximately 5-fold lower affinity for homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRA2 complex recruits the

CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By  
 CC similarity).  
 CC -1- SUBUNIT: Binds to TRAF2 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M50469; AAA39752.1; -;  
 CC EMBL; M59378; AAA40483.1; -;  
 CC EMBL; Y14619; CAA74969.1; -;  
 CC EMBL; Y14620; CAA74969.1; JOINED.  
 CC EMBL; Y14621; CAA74969.1; JOINED.  
 CC EMBL; Y14622; CAA74969.1; JOINED.  
 CC EMBL; Y14623; CAA74969.1; JOINED.  
 CC EMBL; Y14623; CAA74969.1; JOINED.  
 CC EMBL; Y14623; CAA74969.1; JOINED.  
 CC EMBL; U39488; AAA85021.1; -;  
 CC EMBL; X87128; CAA60618.1; -;  
 CC PIR; B38634; B38634.  
 CC DR HSSP; P19438; INCF.  
 CC DR MGD; MGI:1314883; Tnfrsf1b.  
 CC DR GO; GO:0007166; P-cell surface receptor linked signal transdu. .; IMP.  
 CC DR GO; GO:0006954; P:inflammatory response; IMP.  
 CC DR GO; GO:0008220; P:necrosis; IMP.  
 CC DR InterPro; IPR001368; TNFR\_C6.  
 CC DR Pfam; PF00020; TNFR\_C6; 4.  
 CC DR PIRSF; PIRSF001968; TNFR\_2; 1.  
 CC DR SMART; SM00208; TNFR\_4.  
 CC DR PROSITE; PS00852; TNFR\_NGFR\_1; 2.  
 CC DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.  
 CC DR Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 KW SIGNAL 1 22  
 FT CHAIN 23 474 Tumor necrosis factor receptor  
 FT DOMAIN 23 258 superfamily member 1B  
 FT TRANSMEM 259 288 Extracellular (Potential).  
 FT DOMAIN 289 474 Potential.  
 FT REPEAT 39 77 Cytoplasmic (Potential).  
 FT REPEAT 78 119 TNFR-Cys 1.  
 FT REPEAT 120 164 TNFR-Cys 2.  
 FT REPEAT 165 203 TNFR-Cys 3.  
 FT DISULFID 40 54 TNFR-Cys 4.  
 FT DISULFID 55 68 By similarity.  
 FT DISULFID 58 76 By similarity.  
 FT DISULFID 79 94 By similarity.  
 FT DISULFID 97 111 By similarity.  
 FT DISULFID 101 119 By similarity.  
 FT DISULFID 121 127 By similarity.  
 FT DISULFID 136 145 By similarity.  
 FT DISULFID 139 163 By similarity.  
 FT DISULFID 166 181 By similarity.  
 FT CARBOHYD 69 69 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 195 195 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 78 78 D -> DSDTVCAD (in Ref. 3).  
 FT CONFLICT 102 102 T -> S (in Ref. 3).  
 FT CONFLICT 108 108 I -> T (in Ref. 3).  
 FT CONFLICT 283 283 I -> F (in Ref. 3).  
 FT CONFLICT 331 331 S -> SS (in Ref. 3).  
 FT CONFLICT 360 360 F -> S (in Ref. 3).  
 FT CONFLICT 436 436 C -> Y (in Ref. 3).  
 SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;  
 Query Match 14.3%; Score 312; DB 1; Length 474;  
 Best Local Similarity 34.3%; Pred. No. 1.6e-13;  
 Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;  
 QY 5 LCCALLVLLDIEWTQTETLPKYL--HYDPETH-----QLLCKKCAPGTY 49



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 83.8966 Seconds  
(without alignments)  
1843.986 Million cell updates/sec

Title: US-09-389-782A-5  
Perfect score: 2240  
Sequence: 1 ETTPPKYLHYDEETSHQLLC.....VMHEALHNHYTQKLSLSLSPG 400

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1980s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2240	100.0	400	4	AAB80901	Human OPG
2	2240	100.0	400	4	AAY72919	Human OPG
3	2240	100.0	422	4	AAB66993	OPG-Fc. 4
4	2227	99.4	406	4	AAB80902	Human OPG
5	2227	99.4	406	4	AAY72920	Human OPG
6	2225	99.3	425	5	ABG71831	Human OPG
7	2222.5	99.2	407	4	AAB80899	Human OPG
8	2222.5	99.2	407	4	AAY72917	Human ost
9	2218.5	99.0	413	4	AAB80900	Human OPG
10	2218.5	99.0	413	4	AAY72918	Human ost
11	2191	97.8	404	4	AAB80903	Human OPG
12	2191	97.8	404	4	AAY72921	Human OPG
13	1522.5	68.0	659	6	ABJ37103	Concatame
14	1522.5	68.0	659	8	ADQ79910	Human tum
15	1517	67.7	489	8	ADM32913	Amino aci
16	1514.5	67.6	490	6	ABJ37099	Concatame
17	1514.5	67.6	490	8	ADQ79902	Human tum
18	1514.5	67.6	720	6	ABJ37101	Concatame
19	1514.5	67.6	720	8	ADQ79906	Human tum
20	1502	67.1	518	4	AAB50080	TNFR:Fc f
21	1502	67.1	518	4	AAB70001	stTNFR1075
22	1493	66.7	485	2	AAR24016	Fusion pr
23	1490.5	66.5	450	7	ADL06639	stNPR1:1
24	1488	66.4	518	2	AAR51003	Sequence
25	1471.5	65.7	440	7	ADJ66000	Herpes vi

26	1471.5	65.7	440	8	ADP03589	Adp03589 Infection
27	1463	65.3	439	8	ADO47876	Ado47876 Alpha-Her
28	1461.5	65.2	443	6	ABP58181	Abp58181 Human RAN
29	1461.5	65.2	443	6	AAE34361	Aae34361 Human RAN
30	1459.5	65.2	444	5	ABG71833	Abg71833 RANK bind
31	1422.5	63.5	442	7	ADB17001	Adb17001 Human RAN
32	1422.5	63.5	443	7	ADB17002	Adb17002 Human RAN
33	1422	63.5	443	7	ADB17000	Adb17000 Murine RA
34	1392.5	62.2	608	6	ABJ37102	Abj37102 Concatame
35	1392.5	62.2	608	8	ADQ79908	Adq79908 Human tum
36	1384.5	61.8	444	6	ABJ37098	Abj37098 Concatame
37	1384.5	61.8	444	8	ADQ79900	Adq79900 Human tum
38	1384.5	61.8	628	6	ABJ37100	Abj37100 Concatame
39	1384.5	61.8	628	8	ADQ79904	Adq79904 Human tum
40	1352	60.4	376	2	AAW60037	Aaw60037 Antigenic
41	1350.5	60.3	396	8	ADP57557	Adp57557 Mouse ymk
42	1345.5	60.1	398	7	ABW02717	Abw02717 Mouse tms
43	1345.5	60.1	398	8	ADJ45758	Adj45758 Murine tm
44	1341.5	59.9	445	7	ADL06637	Adl06637 sTNFR1:1g
45	1337	59.7	376	2	AAW50287	Aaw50287 Human Fas

ALIGNMENTS

RESULT 1  
AAB80901  
ID AAB80901 standard; protein; 400 AA.  
XX  
AC AAB80901: 1 4  
XX  
DT 31-MAY-2001 (first entry)  
XX  
DE Human OPG(22-194)-FcdeltaC fusion protein.  
XX  
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;  
KW osteoclast formation inhibition; bone resorption inhibition;  
KW immunoglobulin.  
XX  
OS Homo sapiens.  
XX  
PN WO200117543-A2.  
XX  
PD 15-MAR-2001.  
XX  
PF 18-AUG-2000; 2000WO-US022806.  
XX  
PR 03-SEP-1999; 99US-00389545.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Dunstan CR;  
XX  
DR WPI; 2001-265936/27.  
XX  
PT Preventing or treating lytic bone diseases, particularly associated with  
PT cancer or metastasis, by administering an osteoprotegrin polypeptide.  
XX  
PS Claim 11; Fig 5; 87pp; English.

The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophogeal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic

CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
 CC or treatment of loss of bone mass, which occurs in conditions including  
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome), and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteoclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating  
 CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and  
 CC CH3 regions; see AAB80897-8)

XX  
 SQ Sequence 400 AA;

Query Match 100.0%; Score 2240; DB 4; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 3e-130;  
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVKCELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 120  
 DB 61 YCSPVKCELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 120  
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDKTHTC 180  
 DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDKTHTC 180  
 QY 181 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPVKFNWYVDGVEVHN 240  
 DB 181 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPVKFNWYVDGVEVHN 240  
 QY 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPLEKTIISKAKGPREP 300  
 DB 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPLEKTIISKAKGPREP 300  
 QY 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFEL 360  
 DB 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFEL 360  
 QY 361 YSKLTVDKSRWQGNVFCFSVMHEALHNYHTQKSLSPG 400  
 DB 361 YSKLTVDKSRWQGNVFCFSVMHEALHNYHTQKSLSPG 400

## RESULT 2

AA72919  
 ID AAY72919 standard; protein; 400 AA.  
 XX  
 AC AAY72919;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX Human OPG (22-194 aa)-Fc region (lacking 1-5 residues) fusion protein.

XX Human: fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 KW periodontal.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .173  
 FT /note= "Derived from human osteoprotegerin fragment (22-  
 FT 194 residues)"  
 FT Region 174  
 FT /label= Linker  
 FT Region 175. .400  
 FT /note= Human IgG1 Fc region lacking 1-5 residues  
 WO200118203-A1.  
 XX 15-MAR-2001.  
 XX 18-AUG-2000; 2000WO-US022797.  
 XX 03-SEP-1999; 99US-00389782.  
 XX (AMGE-) AMGEN INC.  
 XX Dunstan CR, Wooden SK, Mann MB;  
 XX WPI; 2001-244572/25.  
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
 PT by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 XX Claim 7; Fig 5; 119pp; English.  
 PS The present sequence is a fusion protein comprising a sequence derived  
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with  
 CC human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues by a  
 CC linker. OPG negatively regulates the formation of osteoclasts in vitro  
 CC and in vivo. It blocks the differentiation of osteoclasts from monocyte  
 CC or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion  
 CC protein is administered for the treatment of bone loss resulting from  
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia  
 CC associated with surgery or steroid administration, osteonecrosis, bone  
 CC loss due to rheumatoid arthritis, periodontal bone loss, osteolytic  
 CC metastasis and/or prosthetic loosening  
 XX Sequence 400 AA;

Query Match 100.0%; Score 2240; DB 4; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 3e-130;  
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETFPPKYLHYDEETSHQLLCKDPCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVKCELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 120  
 DB 61 YCSPVKCELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVGAGTPERNTV 120  
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDKTHTC 180  
 DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDKTHTC 180  
 QY 181 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPVKFNWYVDGVEVHN 240  
 DB 181 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPVKFNWYVDGVEVHN 240  
 QY 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPLEKTIISKAKGPREP 300  
 DB 241 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPLEKTIISKAKGPREP 300

Db 241 AKTKPREQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGPREP 300  
Qy 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 360  
Db 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 360  
Qy 361 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPG 400  
Db 361 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPG 400

RESULT 3  
AAB66993  
ID AAB66993 standard; protein; 422 AA.  
XX AC AAB66993;  
XX XX  
DT 19-APR-2001 (first entry)  
XX DE  
DE OPF-Pc.  
XX KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
KW ischaemia; Parkinson's disease.  
XX KW  
OS Unidentified.  
XX XX  
PN WO20103719-A2.  
XX PD  
XX PD 18-JAN-2001.  
XX PF 07-JUL-2000; 2000WO-US018667.  
XX PR 09-JUL-1999; 99US-00350670.  
XX PR 09-DEC-1999; 99US-00457647.  
XX XX  
PA (AMGE-) AMGEN INC.  
XX XX  
XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;  
PI WPI; 2001-103031/11.  
XX DR N-PSDB; AAF57869.  
XX DR  
XX  
PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
PT multiple sclerosis and asthma, comprises administering an osteoprotegerin  
PT protein in conjunction with e.g. inhibitors of interleukin and tumor  
PT necrosis factor alpha.  
XX XX  
XX Disclosure; Fig 29; 316pp; English.  
XX XX  
CC The present invention relates to a method for treating conditions leading  
CC to bone loss. The method comprises administering a purified and isolated  
CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)  
CC in conjunction with other substances such as tumour necrosis factor-alpha  
CC (TNF-alpha) inhibitors, interleukin (IL)-6 -8 and -18 inhibitors, ICE  
CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet  
CC activating factor (PAF) antagonists. The method is useful for treating  
CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
CC graft-versus-host disease (GVHD). Other diseases that can be treated  
CC include acute pancreatitis, Alzheimer's disease, anorexia,  
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
CC psoriasis and septic shock  
XX XX  
SQ Sequence 422 AA;

Query Match 100.0%; Score 2240; DB 4; Length 422;  
Best Local Similarity 100.0%; Pred. No. 3.2e-130; Indels 0; Gaps 0;  
Matches 400; Conservative 0; Mismatches 0;  
Qy 1 ETFFPKYLHYDETSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSMHTSDECL 60  
Db 22 ETFFPKYLHYDETSQQLCDKCPGTYLKQHTAKWKTVCAPCPDHYTDSMHTSDECL 81  
Qy 61 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKXRSCTPPGFGVVQAGTPERTV 120  
Db 82 YCSPVKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKXRSCTPPGFGVVQAGTPERTV 141  
Qy 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNCNSNSTOKVDKTHTC 180  
Db 142 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNCNSNSTOKVDKTHTC 201  
Qy 181 PPCAPELGGPSVFLFPFKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 240  
Db 202 PPCAPELGGPSVFLFPFKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 261  
Qy 241 AKTKPREQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGPREP 300  
Db 262 AKTKPREQNSTYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGPREP 321  
Qy 301 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 360  
Db 322 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 381  
Qy 361 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPG 400  
Db 382 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPG 421

RESULT 4  
AAB80902  
ID AAB80902 standard; protein; 406 AA.  
XX AC AAB80902;  
XX DT 31-MAY-2001 (first entry)  
XX DE Human OPG(22-201)-FcdeltaC fusion protein.  
XX KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;  
KW osteoclast formation inhibition; bone resorption inhibition;  
KW immunoglobulin.  
XX OS Homo sapiens.  
XX PN WO200117543-A2.  
XX PD 15-MAR-2001.  
XX PF 18-AUG-2000; 2000WO-US022806.  
XX PR 03-SEP-1999; 99US-00389545.  
XX PA (AMGE-) AMGEN INC.  
XX PI Dunstan CR;  
XX DR WPI; 2001-265936/27.  
XX PT Preventing or treating lytic bone diseases, particularly associated with  
XX cancer or metastasis, by administering an osteoprotegrin polypeptide.  
XX Disclosure; Fig 6; 87pp; English.  
XX The present invention relates to a method for the prevention or treatment  
XX of lytic bone disease or multiple myeloma. Also the method can be used  
XX for preventing metastasis of cancer to bone or osteosclerotic bone  
XX metastasis. The method comprises administering an OPG (osteoprotegrin)

CC polypeptide or OPG fusion protein. The present sequence is one such OPG  
 CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone  
 CC resorption) by blocking differentiation from monocytes/macrophage  
 CC precursors. The OPG polypeptide can be used in a method of preventing or  
 CC treating lytic bone disease, for preventing metastasis of cancer to bone  
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
 CC rectal, bladder, cervical, ovarian, liver, and preventing the gastrointestinal  
 CC tract, multiple myeloma or lymphoma) and preventing the osteoclastotic  
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
 CC or treatment of loss of bone mass, which occurs in conditions including  
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteoclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating  
 CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the FC region of immunoglobulin IgGgamma1 (the hinge, CH2 and  
 CC CH3 regions; see AAB0897-8)  
 XX  
 SQ Sequence 406 AA;

Query Match 99.4%; Score 2227; DB 4; Length 406;  
 Best Local Similarity 98.5%; Pred. No. 2e-129;  
 Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;  
 QY 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 Db 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVKELQYVKECNTRNHRVCEKGRYLEIEFCLKHKRSCPPGFGVVOAGTPERTNV 120  
 Db 61 YCSPVKELQYVKECNTRNHRVCEKGRYLEIEFCLKHKRSCPPGFGVVOAGTPERTNV 120  
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQK-----V 174  
 Db 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTV 180  
 QY 175 DKHTHCPCPAPELLGGPSVFLFPKPKDLMISTPVTCTVVDVSHEDPVKNWYVD 234  
 Db 181 DKHTHCPCPAPELLGGPSVFLFPKPKDLMISTPVTCTVVDVSHEDPVKNWYVD 240  
 QY 235 GVEVHNATKPREQYNSTYRVVSVLTVLHQLNGKVKCKVSNKALPAPEKTIISKAK 294  
 Db 241 GVEVHNATKPREQYNSTYRVVSVLTVLHQLNGKVKCKVSNKALPAPEKTIISKAK 300  
 QY 295 GQPREFQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 354  
 Db 301 GQPREFQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360  
 QY 355 DGSFFLYSKLTVDKSRWQQGNVFCVMVHEALHNHYTQKSLSLSPG 400  
 Db 361 DGSFFLYSKLTVDKSRWQQGNVFCVMVHEALHNHYTQKSLSLSPG 406

RESULT 5

AAV72920  
 ID AAV72920 standard; protein; 406 AA.  
 XX  
 AC AAV72920;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX  
 DE Human OPG (22-201 aa)-Fc region (lacking 1-5 residues) fusion protein.  
 XX  
 KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 KW periodontal.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..179  
 FT /note= "Derived from human osteoprotegerin fragment (22-  
 FT 201 residues)"  
 FT Region 180  
 FT /label= Linker  
 FT Region 181..406  
 FT /note= Human IgG1 Fc region lacking 1-5 residues;  
 FT (Corresponds to 6-231 residues of IgG1 Fc region)  
 XX  
 PN WO200118203-A1.  
 PD 15-MAR-2001.  
 PF 18-AUG-2000; 2000WO-US022797.  
 PR 03-SEP-1999; 99US-00389782.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Dunstan CR, Wooden SK, Mann MB;  
 DR WPI; 2001-244572/25.  
 XX  
 PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
 PT by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 XX  
 PS Claim 7; Fig 6; 119pp; English.  
 XX  
 CC The present sequence is a fusion protein comprising a sequence derived  
 CC from human osteoprotegerin (OPG; 22-201 residues) which is fused with  
 CC human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues, by a  
 CC linker. OPG negatively regulates the formation of osteoclasts in vitro  
 CC and in vivo. It blocks the differentiation of osteoclasts from monocyte  
 CC or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion  
 CC protein is administered for the treatment of bone loss resulting from  
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia  
 CC associated with surgery or steroid administration, osteonecrosis, bone  
 CC loss due to rheumatoid arthritis, periodontal bone loss, osteolytic  
 CC metastasis and/or prosthetic loosening  
 XX  
 SQ Sequence 406 AA;

Query Match 99.4%; Score 2227; DB 4; Length 406;  
 Best Local Similarity 98.5%; Pred. No. 2e-129;  
 Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;  
 QY 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 Db 1 ETFFPKYLHYDEETSHOLLCDKCPGTYLKQCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVKELQYVKECNTRNHRVCEKGRYLEIEFCLKHKRSCPPGFGVVOAGTPERTNV 120  
 Db 61 YCSPVKELQYVKECNTRNHRVCEKGRYLEIEFCLKHKRSCPPGFGVVOAGTPERTNV 120  
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQK-----V 174

Db 121 CKRCPDGFPSNETSSKAPCKKHTNCSVFGLLLTQKGNATHDNCNSNSTQKCGIDVTV 180  
Qy 175 DKHTTCCPCAPAPLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234  
Db 181 DKHTTCCPCAPAPLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240  
Qy 235 GVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 294  
Db 241 GVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 300  
Qy 295 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 354  
Db 301 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360  
Qy 355 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPG 400  
Db 361 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPG 406

RESULT 6  
ABG71831  
ID ABG71831 standard; protein; 425 AA.  
AC ABG71831;  
XX  
XX  
DT 14-APR-2003 (first entry)  
DE Human OPG protein for expression in mammalian cells.  
DE  
XX  
XX  
KW RANKL; human receptor activator of NFkappaB; osteoprotegerin; OPG;  
KW RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;  
KW osteoporosis; bone disease; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
PN WO00264782-A2.  
PD 22-AUG-2002.  
XX  
XX  
PP 08-FEB-2002; 2002WO-DK000090.  
XX  
PR 09-FEB-2001; 2001DK-00000214.  
PR 09-FEB-2001; 2001US-0267843P.  
PR 23-MAR-2001; 2001DK-00000498.  
PR 23-MAR-2001; 2001US-0278320P.  
XX  
XX  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
XX  
PI Haaning JM, Halkier T;  
PI  
XX  
XX  
DR WPI: 2002-691592/74.  
DR N-PSDB; ABS56347.  
XX  
XX  
PT Novel human receptor activator of NFkappaB (hRANK) or human  
PT osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand  
PT (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for  
PT treating osteoporosis.  
XX  
XX  
PS Example 4; Fig 12; 129pp; English.

CC This invention relates to a novel polypeptide having an amino acid  
CC sequence that is different from and is at least about 70% identical to  
CC the amino acid sequence of human receptor activator of NFkappaB (hRANK)  
CC or human osteoprotegerin (hOPG), and which has a binding affinity to RANK  
CC ligand (RANKL) that is at least as high as the binding affinity of hRANK  
CC or hOPG to RANKL, as determined by functional competition assay. The  
CC protein of the invention may have osteopathic activity and may act as a  
CC RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity  
CC inhibitor. The nucleotide sequence shown in the invention may be used in  
CC gene therapy. The protein of the invention or fusion proteins comprising  
CC this protein are useful as a pharmaceutical, and in the preparation of a

CC medicament for treating or preventing osteoporosis, or other bone  
CC diseases or diseases associated with binding of RANKL to the RANK  
CC receptor. A host cell containing a vector expressing the protein is  
CC useful for producing a polypeptide having binding affinity to RANKL,  
CC where the polypeptide comprises at least one N- or O-glycosylation site  
CC and the host cell is a eukaryotic host cell capable of in vivo  
CC glycosylation, and/or the polypeptide is subjected to conjugation to a  
CC non-polypeptide moiety in vitro. The protein of the invention has  
CC increased functional in vivo half-life and/or serum half-life compared to  
CC hRANK or hOPG and has an improved binding affinity to RANKL compared to  
CC the binding affinity of hRANK or hOPG to RANKL, as determined by a  
CC functional competition assay. The present sequence represents a human OPG  
CC protein modified for expression in a mammalian system, this sequence has  
CC the human OPG protein fused to a leu-Glu dipeptide and amino acid  
CC residues 247-475 of human IgG1  
XX  
XX  
SQ Sequence 425 AA;  
Query Match 99.3%; Score 2225; DB 5; Length 425;  
Best Local Similarity 98.8%; Pred. No. 2.7e-129;  
Matches 399; Conservative 1; Mismatches 0; Indels 4; Gaps 1;  
Qy 1 ETTPPKYLHYDEETSHQLLCKDCKPPGTYLKQHTAKWTVCAPCPDHYTDSMHTSDECL 60  
Db 22 ETTPPKYLHYDEETSHQLLCKDCKPPGTYLKQHTAKWTVCAPCPDHYTDSMHTSDECL 81  
Qy 61 YCSPVKELQYVKQECNRTNHRVCEKGRYLEIEFCLKXRSCTPPGFGVVGAGTPTERTV 120  
Db 82 YCSPVKELQYVKQECNRTNHRVCEKGRYLEIEFCLKXRSCTPPGFGVVGAGTPTERTV 141  
Qy 121 CKRCPDGFPSNETSSKAPCKKHTNCSVFGLLLTQKGNATHDNCNSNSTQKVG---DK 176  
Db 142 CKRCPDGFPSNETSSKAPCKKHTNCSVFGLLLTQKGNATHDNCNSNSTQKLEKSSDK 201  
Qy 177 THTCPCAPAPLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 236  
Db 202 THTCPCAPAPLLGSPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 261  
Qy 237 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAGQ 296  
Db 262 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAGQ 321  
Qy 297 PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 356  
Db 322 PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 381  
Qy 357 SFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPG 400  
Db 382 SFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPG 425

RESULT 7  
AAB80899  
ID AAB80899 standard; protein; 407 AA.  
XX  
AC AAB80899;  
XX  
DT 31-MAY-2001 (first entry)  
XX  
XX  
DE Human OPG(22-194)-Fc fusion protein.  
XX  
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
KW multiple myeloma; osteoclastotic bone metastasis; OPG; osteoprotegerin;  
KW osteoclast formation inhibition; bone resorption inhibition;  
XX immunoglobulin.  
OS Homo sapiens.  
XX  
XX WO200117543-A2.  
XX  
XX  
PD 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.  
 XX (AMGE-) AMGEN INC.  
 XX Dunstan CR;  
 XX WPI; 2001-265936/27.  
 XX Preventing or treating lytic bone diseases, particularly associated with  
 XX cancer or metastasis, by administering an osteoprotegerin polypeptide.  
 XX Disclosure; Fig 3; 87pp; English.  
 XX The present invention relates to a method for the prevention or treatment  
 XX of lytic bone disease or multiple myeloma. Also the method can be used  
 XX for preventing metastasis of cancer to bone or osteosclerotic bone  
 XX metastasis. The method comprises administering an OPG (osteoprotegerin)  
 XX polypeptide or OPG fusion protein. The present sequence is one such OPG  
 XX fusion protein. OPG inhibits formation of osteoclasts (and thus bone  
 XX resorption) by blocking differentiation from monocytes/macrophage  
 XX precursors. The OPG polypeptide can be used in a method of preventing or  
 XX treating lytic bone disease, for preventing metastasis of cancer to bone  
 XX (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
 XX rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal  
 XX tract, multiple myeloma or lymphoma) and preventing the osteosclerotic  
 XX bone metastasis. The OPG fusion polypeptides are used in the prevention  
 XX or treatment of loss of bone mass, which occurs in conditions including  
 XX osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 XX (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 XX congenital forms of osteoporosis (osteogenesis imperfecta,  
 XX homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 XX due to immobilisation of extremities; Paget's disease of bone (osteitis  
 XX deformingans) in adults and juveniles; osteomyelitis, or an infectious  
 XX lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 XX and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 XX leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 XX hyperthyroidism and renal function disorders; osteopaenia following  
 XX surgery, induced by steroid administration, and associated with disorders  
 XX of the small and large intestine and with chronic hepatic and renal  
 XX diseases; osteonecrosis, or bone cell death, associated with traumatic  
 XX injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 XX cell anaemia, systemic lupus erythematosus and other conditions; bone  
 XX loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 XX prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 XX are also used in the replacement of structurally sound bone with  
 XX disorganised bone as seen in Paget's disease of bone (osteitis deformingans)  
 XX in adults and juveniles; hyperparathyroidism, in congenital bone  
 XX disorders such as fibrous dysplasia, and in osteosclerotic bone  
 XX metastases. The OPG fusion proteins can exhibit increased circulating  
 XX half-lives and slower clearance times, thereby providing a more sustained  
 XX activity. The OPG fusion protein comprises a fragment of the human OPG  
 XX protein and the FC region of immunoglobulin IgGgamma1 (the hinge, CH2 and  
 XX CH3 regions; see AAB80897-8)  
 XX Sequence 407 AA;

Query Match 99.2%; Score 2222.5; DB 4; Length 407;  
 Best Local Similarity 98.0%; Pred. No. 3,7e-129;  
 Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 ETPFPKYLHYDETSHQLCDKCPGTYLKQCTAKWTKVCAPCDPHYTDSWHTSDCL 60  
 DB 1 ETPFPKYLHYDETSHQLCDKCPGTYLKQCTAKWTKVCAPCDPHYTDSWHTSDCL 60  
 QY 61 YCSPVKELQYVKQCNTHNRVCSCKGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120  
 DB 61 YCSPVKELQYVKQCNTHNRVCSCKGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120  
 QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSSESTQKV----- 174  
 DB 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSSESTQKAAAEPS 180

QY 175 -DKTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYV 233  
 DB 181 CDKTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYV 240  
 QY 234 DGVFVHNATKPREQYNSYTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKA 293  
 DB 241 DGVFVHNATKPREQYNSYTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKA 300  
 QY 294 KGQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVEWESNGOPENNYKTTTPPVLD 353  
 DB 301 KGQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVEWESNGOPENNYKTTTPPVLD 360  
 QY 354 SDGSFFLYSKLTVDKSRMQQGNVFCVSMVHEALHNYTKQSLSLSPG 400  
 DB 361 SDGSFFLYSKLTVDKSRMQQGNVFCVSMVHEALHNYTKQSLSLSPG 407  
 RESULT 8  
 AAY72917  
 ID AAY72917 standard; protein; 407 AA.  
 XX AC AAY72917;  
 XX DT 13-JUN-2001. (first entry)  
 XX Human osteoprotegerin (22-194 residues)-IgG1 FC region fusion protein.  
 XX Human; fusion protein; osteoprotegerin; OPG; FC protein; osteopathic;  
 XX therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 XX hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 XX osteolytic metastasis; prostatic loosening; immunoglobulin G1; IgG1;  
 XX periodontal.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Region 1..173  
 FT /note= "Derived from human osteoprotegerin fragment (22-  
 FT 194 residues)"  
 FT Region 174..176  
 FT /label= Linker  
 FT Region 177..407  
 FT /label= Human\_IgG1\_FC\_region  
 WO200118203-A1.  
 PD 15-MAR-2001.  
 PF 18-AUG-2000; 2000WO-US022797.  
 PR 03-SEP-1999; 99US-00389782.  
 PA (AMGE-) AMGEN INC.  
 XX Dunstan CR, Wooden SK, Mann MB;  
 DR WPI; 2001-244572/25.  
 XX Osteoprotegerin-FC protein fusions useful for treating bone loss caused  
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 PS Example 1; Fig 3; 119pp; English.  
 XX The present sequence is a fusion protein comprising a sequence derived  
 XX from human osteoprotegerin (OPG; 22-194 residues) which is fused with  
 XX human immunoglobulin G1 (IgG1) FC region by a linker. OPG negatively  
 XX regulates the formation of osteoclasts in vitro and in vivo. It blocks  
 XX the differentiation of osteoclasts from monocyte or macrophage precursors  
 XX and the reabsorption of bone. The OPG-FC fusion protein is administered  
 XX for the treatment of bone loss resulting from osteoporosis, Paget's  
 XX disease, osteomyelitis, hypercalcaemia, osteopenia associated with  
 XX surgery or steroid administration, osteonecrosis, bone loss due to  
 XX rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or

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CC prosthetic loosening
XX Sequence 407 AA;
SQ
  Query Match          99.2%; Score 2222.5; DB 4; Length 407;
  Best Local Similarity 98.0%; Pred. No. 3.7e-129;
  Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 1 ETFPKYLHYDETSKQPCPPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETFPKYLHYDETSKQPCPPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVKECNRTNHRVCECKEGRYLIEFCLKHRSCTPPGFGVQAGTPERTV 120
DB 61 YCSPVCKELQYVKECNRTNHRVCECKEGRYLIEFCLKHRSCTPPGFGVQAGTPERTV 120
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSESTQKV----- 174
DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSESTQKAAEPKS 180
QY 175 -DKTHTCCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYV 233
DB 181 CDKTHCTCCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYV 240
QY 234 DGEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA 293
DB 241 DGEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKA 300
QY 294 KGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 353
DB 301 KGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360
QY 354 SDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSPG 400
DB 361 SDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSPG 407

RESULT 9
AAB80900
ID AAB80900 standard; protein; 413 AA.
XX
AC AAB80900;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human OPG(22-201)-Fc fusion protein.
XX
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.
XX
OS Homo sapiens.
XX
PN WO200117543-A2.
XX
XX 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022806.
XX
PR 03-SBP-1999; 99US-00389545.
XX
XX (AMGE-) AMGEN INC.
XX
XX Dunstan CR;
XX
XX WPI; 2001-265936/27.
XX
XX Preventing or treating lytic bone diseases, particularly associated with
XX cancer or metastasis, by administering an osteoprotegrin polypeptide.
XX
XX Disclosure; Fig 4; 87pp; English.
XX

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CC The present invention relates to a method for the prevention or treatment
CC of lytic bone disease or multiple myeloma. Also the method can be used
CC for preventing metastasis of cancer to bone or osteosclerotic bone
CC metastasis. The method comprises administering an OPG (osteoprotegrin)
CC polypeptide or OPG fusion protein. The present sequence is one such OPG
CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
CC resorption) by blocking differentiation from monocytes/macrophage
CC precursors. The OPG polypeptide can be used in a method of preventing or
CC treating lytic bone disease, for preventing metastasis of cancer to bone
CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
CC bone metastasis. The OPG fusion polypeptides are used in the prevention
CC or treatment of loss of bone mass, which occurs in conditions including
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
CC congenital forms of osteoporosis (osteogenesis imperfecta,
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and bone
CC due to immobilisation of extremities; Paget's disease of bone (osteitis
CC deformans) in adults and juveniles; osteomyelitis, or an infectious
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
CC hyperthyroidism and renal function disorders; osteopaenia following
CC surgery, induced by steroid administration, and associated with disorders
CC of the small and large intestine and with chronic hepatic and renal
CC diseases; osteonecrosis, or bone cell death, associated with traumatic
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
CC cell anaemia, systemic lupus erythematosus and other conditions; bone
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
CC are also used in the replacement of structurally sound bone with
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
CC in adults and juveniles; hyperparathyroidism, in congenital bone
CC disorders such as fibrous dysplasia, and in osteosclerotic bone
CC metastases. The OPG fusion proteins can exhibit increased circulating
CC half-lives and slower clearance times, thereby providing a more sustained
CC activity. The OPG fusion protein comprises a fragment of the human OPG
CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
CC CH3 regions; see AAB80897-8)
XX
SQ Sequence 413 AA;
  Query Match          99.0%; Score 2218.5; DB 4; Length 413;
  Best Local Similarity 96.6%; Pred. No. 6.7e-129;
  Matches 399; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

QY 1 ETFPKYLHYDETSKQPCPPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETFPKYLHYDETSKQPCPPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVKECNRTNHRVCECKEGRYLIEFCLKHRSCTPPGFGVQAGTPERTV 120
DB 61 YCSPVCKELQYVKECNRTNHRVCECKEGRYLIEFCLKHRSCTPPGFGVQAGTPERTV 120
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSESTQK----- 173
DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTKQGNATHDNCISGNSESTQKIGIDVTA 180
QY 174 -----VDKTHCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEV 227
DB 181 AAEPKSCDKTHTCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEV 240
QY 228 KFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 287
DB 241 KFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 300
QY 288 KTISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 347
DB 301 KTISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 360
QY 348 TTPVLDSDGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKLSLSPG 400

```



CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteoclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating  
 CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and  
 CC CH3 regions; see AAB80897-8)

XX  
 SQ Sequence 404 AA;

Query Match 97.8%; Score 2191; DB 4; Length 404;  
 Best Local Similarity 97.8%; Pred. No. 3.2e-127;  
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;  
 QY 1 ETFPPKYLHYDETSHTQLLCKDCPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 Db 1 ETFPPKYLHYDETSHTQLLCKDCPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERNTV 120  
 Db 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERNTV 120  
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSGSESTQKV---DK 176  
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSGSESTQKSGGGGG 180  
 QY 177 THTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 236  
 Db 181 GGTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240  
 QY 237 EVHNAKTPREEQYNSTYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQ 296  
 Db 241 EVHNAKTPREEQYNSTYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQ 300  
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 Db 301 PREPQVYTLPPSRDELTKQVSLTCLVKGYFSDIAVFNESGQENNYKTTTPVLDSG 360  
 QY 357 SFPLYSKLTVDKSRWQGNVFCVSMHEALHNYTKQSLSLSPG 400  
 Db 361 SFPLYSKLTVDKSRWQGNVFCVSMHEALHNYTKQSLSLSPG 404

RESULT 12  
 AAY72921

ID AAY72921 standard; protein; 404 AA.

XX AAY72921;

XX 13-JUN-2001 (first entry)

XX Human OPG (22-194 residues)-FCG10 fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 XX periodontal.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .173  
 FT /note= "Derived from human osteoprotegerin fragment (22-  
 FT 194 residues)"  
 FT Region 174. .182  
 FT /label= Ser-(Gly)8 linker  
 FT Region 183. .404  
 FT /note= Corresponds to 10-231 residues of human IgG1 Fc  
 FT region  
 PN WO200118203-A1.  
 XX 15-MAR-2001.  
 XX 18-AUG-2000; 2000WO-US022797.  
 XX 03-SEP-1999; 99US-00389782.  
 XX (AMGE-) AMGEN INC.  
 XX Dunstan CR, Wooden SK, Mann MB;  
 XX WPI; 2001-244572/25.

DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 XX Claim 7; Fig 7; 119pp; English.  
 XX The present sequence is a fusion protein comprising a sequence derived  
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with  
 CC human immunoglobulin G1 (IgG1) FcG10 region (lacks 1-9 residues and has a  
 CC Ser-(Gly)8 linker). OPG negatively regulates the formation of osteoclasts  
 CC in vitro and in vivo. It blocks the differentiation of osteoclasts from  
 CC monocyte or macrophage precursors and the reabsorption of bone. The OPG-  
 CC Fc fusion protein is administered for the treatment of bone loss  
 CC resulting from osteoporosis, Paget's disease, osteomyelitis,  
 CC hypercalcaemia, osteopenia associated with surgery or steroid  
 CC administration, osteonecrosis, bone loss due to rheumatoid arthritis,  
 CC periodontal bone loss, osteolytic metastasis and/or prosthetic loosening

XX Sequence 404 AA;

Query Match 97.8%; Score 2191; DB 4; Length 404;  
 Best Local Similarity 97.8%; Pred. No. 3.2e-127;  
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;  
 QY 1 ETFPPKYLHYDETSHTQLLCKDCPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 Db 1 ETFPPKYLHYDETSHTQLLCKDCPPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERNTV 120  
 Db 61 YCSPVKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERNTV 120  
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 QY 177 THTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 236  
 Db 181 GGTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240  
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 Db 241 EVHNAKTPREEQYNSTYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQ 300

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QY 297 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 356
Db 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 360
QY 357 SFELYSKLTVDKSRWQGNVFSVMHEALHNHYTKSLSPG 400
Db 361 SFELYSKLTVDKSRWQGNVFSVMHEALHNHYTKSLSPG 404

RESULT 13
ID ABJ37103 standard; protein; 659 AA.
AC ABJ37103;
XX
XX
DT 08-MAY-2003 (first entry)
DE
DE Concatameric immunoadhesion human protein sequence SEQ ID No 12.
KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.
XX
XX Homo sapiens.
XX
XX WO2003010202-A1.
XX
XX PD 06-FEB-2003.
XX
XX PF 26-JUL-2002; 2002WO-KR001427.
XX
XX PR 26-JUL-2001; 2001KR-00045028.
XX
XX PA (MEDE-) MEDEXGEN CO LTD.
XX
XX PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
XX WPI; 2003-229639/22.
XX
XX DR N-PSDB; ABT32046.
XX
XX PT New concatameric protein having two soluble domains, useful for
XX diagnosing and treating disorders associated with the dimeric protein or
XX its glycosylated form, such as inflammation, septicemia, rheumatoid
XX arthritis and cachexia.
XX
XX PS Claim 27; Page 148-152; 211pp; English.
XX
XX CC The invention relates to a novel concatameric protein comprising two
XX soluble domains, in which an N-terminus of a soluble domain of a
XX biologically active protein is linked to a C-terminus of an identical
XX soluble domain or a different soluble domain of a biologically active
XX protein. The methods and compositions of the present invention are useful
XX for the diagnosis and treatment of disorders associated with dimeric
XX protein or its glycosylated form, such as inflammation, septicemia,
XX cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
XX related diseases. This sequence represents the human concatameric protein
XX of the invention
XX
XX SQ Sequence 659 AA;

Query Match 68.0%; Score 1522.5; DB 6; Length 659;
Best Local Similarity 65.4%; Pred. No. 1e-85;
Matches 295; Conservative 16; Mismatches 75; Indels 65; Gaps 5;

QY 9 HYDETSHOLLCDKCPGPGYLAQHCTAKWTKVCAPCPHYHYTDSWHTSDECLYCSPVCKE 68
Db 214 YFDQ--TAQMCCSKSPGQHAQVCTKTSVTDVCDSCEDSTYQLWNWVPECLSCGRCSS 271
QY 69 LQYVQECNRNTHRVCECKEGRYLBI-----EFLCKHRSCTPPGQVQAGTPPENTVCKE 122
Db 272 DQVETQACTREQNRCTCRPGWYCALSKQEGCLCAPLRCRPGFVGARPGTETSDVCK 331
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QY 123 RCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
Db 332 PCAPGTFSTNTSTIDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPG 387
QY 165 --SGNSESTQ-----KVDKTHCTPCPAPELL 189
Db 388 PVSTRSQHTPTPEPSTAPSTSFLLPMGPPSPAEGSTGDAEPKSCDKTHCTPCPAPELL 447
QY 190 GGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 249
Db 448 GGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 507
QY 250 YNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSR 309
Db 508 YNSTYRVVSVLTVHLQDMLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSR 567
QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGSFYKSLTVDKKS 369
Db 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGSFYKSLTVDKKS 627
QY 370 RWOQGNVFSVMHEALHNHYTKSLSPG 400
Db 628 RWOQGNVFSVMHEALHNHYTKSLSPG 658

RESULT 14
ADQ79910
ID ADQ79910 standard; protein; 659 AA.
XX
XX AC ADQ79910;
XX
XX DT 09-SEP-2004 (first entry)
XX
XX DE Human tumour necrosis factor receptor 2, mgtNFR2-TNFR2/Ig construct.
XX
XX KW Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
XX immunoglobulin; concatameric fused dimer protein; immunoadhesin;
XX Fc fragment; hinge.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PN KR2004009997-A.
XX
XX PD 31-JAN-2004.
XX
XX PF 26-JUL-2002; 2002KR-00045921.
XX
XX PR 26-JUL-2002; 2002KR-00045921.
XX
XX PA (MEDE-) MEDEXGEN INC.
XX
XX PI Choi EY, Han JU, Jung YH, Kim JM, Lee HJ;
XX
XX DR WPI; 2004-458871/43.
XX
XX DR N-PSDB; ADQ79909.
XX
XX PT Concatameric immunoadhesin.
XX
XX PS Claim 27; SEQ ID NO 12; 129pp; Korean.
XX

The invention relates to a concatameric fused dimer protein and
glycosylation modification protein providing concatameric immunoadhesin
with improved efficacy and stability. The concatameric protein is
characteristically formed by binding C-terminal of one biologically
active protein with N-terminal of same or different biologically active
protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
CTLA4. Two monomer proteins which are formed by fusing the extracellular
region of a protein participating in the same immune reaction to an
immunoglobulin Fc fragment, bound together at a hinge region by
disulphide bond to give the concatameric fused dimer protein, wherein the
immunoglobulin is IgG. The present sequence represents a monomeric or
```



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 21.8688 Seconds  
(without alignments)  
1365.399 Million cell updates/sec

Title: US-09-389-782A-5  
Perfect score: 2240  
Sequence: 1 ETPPPKLYHDETSQLLC.....VMHEALHNHYTKSLSLSPG 400

Scoring table: BLOSUM62  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1510.5	67.4	486	1	US-08-243-010-1
2	1502	67.1	518	1	US-08-185-229-4
3	1502	67.1	518	4	US-09-579-845-1
4	1502	67.1	518	4	US-09-579-845-3
5	1352	60.4	360	3	US-09-180-100-11
6	1352	60.4	376	3	US-09-180-100-22
7	1345.5	60.1	398	4	US-09-612-033B-14
8	1332	59.5	438	1	US-08-097-827-11
9	1332	59.5	438	1	US-08-494-574-11
10	1317.5	58.8	424	3	US-09-333-593A-8
11	1266.5	56.5	911	2	US-08-484-438-10
12	1252	55.9	704	4	US-09-590-656-2
13	1252	55.9	704	4	US-09-733-764-2
14	1249.5	55.8	664	3	US-08-957-063-16
15	1249.5	55.8	664	3	US-09-487-685-16
16	1249.5	55.8	664	3	US-08-802-805D-16
17	1249.5	55.8	664	4	US-09-388-316C-16
18	1248.5	55.7	664	3	US-08-957-063-18
19	1248.5	55.7	664	3	US-09-487-685-18
20	1248.5	55.7	664	3	US-08-802-805D-18
21	1248.5	55.7	664	4	US-09-388-316C-18
22	1247	55.7	397	4	US-09-854-864-18
23	1245.5	55.6	283	4	US-09-854-864-9
24	1245.5	55.6	482	3	US-09-189-129-2
25	1245.5	55.6	482	4	US-09-824-286-2
26	1245.5	55.6	680	3	US-08-227-496C-15
27	1244.5	55.6	455	4	US-09-773-877B-24

Sequence 23, Appl  
Sequence 23, Appl  
Sequence 8, Appl  
Sequence 4, Appl  
Sequence 54, Appl  
Sequence 53, Appl  
Sequence 2, Appl  
Sequence 7, Appl  
Sequence 9, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 30, Appl  
Sequence 43, Appl  
Sequence 43, Appl

## ALIGNMENTS

RESULT 1  
US-08-243-010-1  
; Sequence 1, Application US/08243010  
; Patent No. 5639597  
; GENERAL INFORMATION:  
; APPLICANT: Lauffer, Leander  
; APPLICANT: Zettlmeissel, Gerd  
; APPLICANT: Oquendo, Patricia  
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The  
; TITLE OF INVENTION: Production and Use Thereof  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/243,010  
; FILING DATE: 13-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/798,564  
; FILING DATE: 26-NOV-1991  
; APPLICATION NUMBER: DE P 40 37 837.3  
; FILING DATE: 28-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Einaudi, Carol P.  
; REGISTRATION NUMBER: 32,220  
; REFERENCE/DOCKET NUMBER: 02481-1132-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 486 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-243-010-1

Query Match 67.4%; Score 1510.5; DB 1; Length 486;  
Best Local Similarity 65.2%; Pred. No. 1.4e-118;

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Qy	69	LQVVKQECNTHNRVC	CKEGRYLEI-----	BFCLKHRS	CPGFGVVOAGTPE	122			
		:	:	:	:				
Db	103	DQVETQACTREQNRI	CTCRFGWYCALSK	QGGRCLCAPLRCR	PGFGVAREGTETSD	162			
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Qy	123	RCPDGPFNSNTSSK	APCRKHTNCSV	FGLLTQKNATHDNI	CSGNS-----	168			
		:	:	:	:				
Db	163	PCAPGTFNSNTSS	TDICRPHQICNNVAI	-----PGNASMD	AVCTSTSPTRSMAP	218			
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Qy	169	-----	-----	-----	ESTQVKDKTHCTPC	192			
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Qy	193	SVFLFPKPKD	TLMI	SRTPEVTCVVDV	SHEDPEVKFNWTV	252			
		:	:	:	:				
Db	279	SVFLFPKPKD	TLMI	SRTPEVTCVVDV	SHEDPEVKFNWTV	338			
		:	:	:	:				
Qy	253	TYRWVSVLTVL	HDWLNKGEYK	CKVSNKALPA	PIEKTIISKAGQ	312			
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Db	339	TYRWVSVLTVL	HQ--WLNKGEYK	CKVSNKALPA	PIEKTIISKAGQ	397			
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		:	:	:	:				
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Db	458	QGNVFCSV	VMHEALHNHYT	OKSLSPG	485				
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; LENGTH: 518 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-385-229-4

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Query Match	67.1%;	Score	1502;	DB	1;	Length	518;
Best Local Similarity	63.8%;	Pred.	No. 7.9e-118;				
Matches	287;	Conservative	21;	Mismatches	78;	Indels	64; Gaps 4;

  

QY	9	HYDEETSHQLLDCDKCPGTYLVKQHCTAKWKTVCAPCPDHYIYTDSDHSTDBCLYCSPVCKE	68
Db	74	YYDQ--TAQWCSCSKSPGOAHKFCTKTSDTVCDSCEDSYTQLNWNVPCLSGSRCSS	131
QY	69	LQVVQECNRTHRVCEKEGRYLEI-----BFLKHRS CPPFGVVGAGTPERNTVTK	122
Db	132	DQVETOACTREQNRICTCRPGMYCALSKOEGCRLCAPLRKCRPFGFVGAREGTETSDVVK	191
QY	123	RCPDGFPSETSSKAPCRKHTWCSEVGLLLTKGNATHDNICSGNS-----	168
Db	192	PCAPGTFSNTTSTDICRPHQICNVVAI----PGNASMDAVCTSTSPTRSMAPCAVHLPO	247
QY	169	-----ESTQKVDKHTHCPPCAPPELLG	190
Db	248	PVSTRSQHTPEPSTAPSTSFLPLPMGPSPPAEGSTGDEPKSCDKTHTCPPCAPPELLG	307
QY	191	GPSVFLLFPKPQDTLMISITPEVTGVVDVSHEDPEVKFNWYVDGEVHNNAKTPREEQY	250
Db	308	GPSVFLLFPKPQDTLMISITPEVTGVVDVSHEDPEVKFNWYVDGEVHNNAKTPREEQY	367
QY	251	NSTYRVVSVLTVLHDWLNGKBKYCKSVSNKALPAPIEKTISSAKGQPRBPQVYTLPPSRD	310
Db	368	NSTYRVVSVLTVLHDWLNGKDQYCKVSNKALPAPMQKTISSAKGQPREPQVYTLPPSRD	427
QY	311	EILTQNQVSLTCLVKGFYPSPDI AVESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR	370
Db	428	EILTQNQVSLTCLVKGFYPPHIAVESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR	487
QY	371	WOQGNVFCSCVMHEALHHNYHTQKSLSLSPG	400
Db	488	WOQGNVFCSCVMHEALHHNYHTOKSLSLSPG	517

RESULT 3  
US-09-579-845-1  
; Sequence 1, Application US/09579845  
; Patent No. 6537540  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; APPLICANT: Stepan, Anthony M.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING  
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED  
; TITLE OF INVENTION: DISORDERS  
; FILE REFERENCE: 226272004420  
; CURRENT APPLICATION NUMBER: US/09/579,845  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/150,688  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-579-845-1

Query Match 67.1%; Score 1502; DB 4; Length 518;  
Best Local Similarity 63.8%; Pred. No. 7.9e-118;  
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;

QY 9 HYDEETSHQLLCDKPPGTYLKHQHTAKWKTCVPCPDHYVTDSWHTSDCYLCSPVCKE 68  
:::|:::  
DB 74 YDYO--TAMCMCKSCPGOHAFVTKTSDTVCDCSEDSTYTOLWNWPECLSCGRCCS 131

```
Qy 69 LQYVQECNTHNRVCECKEGRYLEI-----EFLKHRSCPPGFGVVGAGTPERNTVCK 122
Db 132 DQVETOACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----168
Db 192 PCAPGTFSTNTSSDICTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPCAVHLPO 247
Qy 169 -----ESTQKVDKTHTCPPCPAPPELLG 190
Db 248 PVSTRSQTPTPEPSTAPSTSPFLPMGSPAPBAGSTGDEPKSCDKTHTCPPCPAPPELLG 307
Qy 191 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNHAKTKPREEQY 250
Db 308 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNHAKTKPREEQY 367
Qy 251 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
Qy 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLYKLTVDKSR 370
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLYKLTVDKSR 487
Qy 371 WQGNVFCSCVMHEALHNYHTQKSLSLSPG 400
Db 488 WQGNVFCSCVMHEALHNYHTQKSLSLSPG 517
```

## RESULT 4

US-09-579-845-3

; Sequence 3, Application US/09579845

; Patent No. 6537540

; GENERAL INFORMATION:

; APPLICANT: Burestein, Haim

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED

; TITLE OF INVENTION: DISORDERS

; FILE REFERENCE: 226272004420

; CURRENT APPLICATION NUMBER: US/09/579,845

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-579-845-3

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Query Match 67.18; Score 1502; DB 4; Length 518;
Best Local Similarity 63.84; Pred. No. 7.9e-118;
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;
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Qy 9 HYDEETSHQLLCKDKPCPGTYLKHCTAKWTKVCAPCPDHYVTDSWHTSDDECLYCSPVCKE 68
Db 74 YYDQ--TAQCCCKSCSGQGHAKVFCTKTSYDVCDSCEDSTYTQLNWNVPECLSGSFCSS 131
Qy 69 LQYVQECNTHNRVCECKEGRYLEI-----EFLKHRSCPPGFGVVGAGTPERNTVCK 122
Db 132 DQVETOACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----168
Db 192 PCAPGTFSTNTSSDICTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPCAVHLPO 247
Qy 169 -----ESTQKVDKTHTCPPCPAPPELLG 190
Db 248 PVSTRSQTPTPEPSTAPSTSPFLPMGSPAPBAGSTGDEPKSCDKTHTCPPCPAPPELLG 307
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Qy 191 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNHAKTKPREEQY 250
Db 308 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNHAKTKPREEQY 367
Qy 251 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 310
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
Qy 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLYKLTVDKSR 370
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLYKLTVDKSR 487
Qy 371 WQGNVFCSCVMHEALHNYHTQKSLSLSPG 400
Db 488 WQGNVFCSCVMHEALHNYHTQKSLSLSPG 517
```

## RESULT 5

US-09-180-100-11

; Sequence 11, Application US/09180100

; Patent No. 6306395

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, No. 63063951c

; APPLICANT: NAKAMURA, Shigekazu

; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

; FILE REFERENCE: 1110-207P

; CURRENT APPLICATION NUMBER: US/09/180,100

; EARLIER FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: PCT/JP97/01502

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-180-100-11

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Query Match 60.44; Score 1352; DB 3; Length 360;
Best Local Similarity 67.34; Pred. No. 1.9e-105;
Matches 270; Conservative 15; Mismatches 60; Indels 56; Gaps 9;
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```
Qy 8 LHYDEETSHQLLCKDKPCPGTYLKHCTAKW-KTVCAPCPD-HYVTDSWHTSDDECLYCSPV 65
Db 7 LHHDGQFCHK-----PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCR-L 61
Qy 66 CKELQVVKQES--CNRTHNRVCECKEGRYLEIEFLKHRSCPP-----GFGVVGAGTPERNT 119
Db 62 CDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVC---EHCDCPTCKEHLIKECTLTSTNT 118
Qy 120 VCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTOKVDKHT 179
Db 119 KCKE--EGSRSNEPKS-----CDKHTT 138
Qy 180 CPPCPAPPELLGSPSVLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVH 239
Db 139 CPPCPAPPELLGSPSVLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVH 198
Qy 240 NAKTKEREQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 299
Db 199 NAKTKEREQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 258
Qy 300 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 359
Db 259 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 318
Qy 360 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 400
Db 319 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPG 359
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## RESULT 6

US-09-180-100-22

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; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAKAMURA, No. 630639510
; TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-22

Query Match      60.4%; Score 1352; DB 3; Length 376;
Best Local Similarity 67.3%; Pred. No. 2e-105;
Matches 270; Conservative 15; Mismatches 60; Indels 56; Gaps 9;

QY      8 LHYDETSHQLLDCDKPPGTYLKHCTAKM-KTVCACPD-HYTTDSWHTSDCLYCSVP 65
Db      23 LHHDCQFCHK-----PCPGERKARDCTVNGDEPCVQEGKEYTDKAFSSKRCR-L 77
QY      66 KLEQYVQKQ--CNRTHNRVCBCKEGRYLEIEFCLKHSRCP--EHCDPCTKCEHGIKCTLSNT 119
Db      78 CDEGHLEVEINCTRTQNTKCRCKPNFPCNSTVC---EHCDPCTKCEHGIKCTLSNT 134
QY      120 VKCRCPDGFENSTSSKAPCRKHTNCVFGLLLTQKNATHDNICSGNSESTQKVDKTHT 179
Db      135 KCKE--EGSRNEPKS-----CDKTHT 154
QY      180 CPPCAPPELLGSPVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVGH 239
Db      155 CPPCAPPELLGSPVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVGH 214
QY      240 NAKTKPREQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 299
Db      215 NAKTKPREQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 274
QY      300 PQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 359
Db      275 PQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 334
QY      360 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSLSPG 400
Db      335 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSLSPG 375

RESULT 7
US-09-612-033B-14
; Sequence 14, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sazis, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmet2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

Query Match      60.1%; Score 1345.5; DB 4; Length 398;
Best Local Similarity 67.7%; Pred. No. 7.6e-105;
Matches 264; Conservative 22; Mismatches 59; Indels 45; Gaps 7;

QY      12 EETSHQLLDCDKPPGTYLKHCH-TAKWKTVCACPDHYTTDSWHTSDCLYCSVPCKELQ 70
Db      52 EYWSKDVCKNCAGTFVAPCEIPIHTQGCCKCHGFTTEKNDYLDACILCS-TCDKQD 110
QY      71 YVQECNTRHNRVCBCKEGRYLEIEFCLKHSRCPFGVQAGTPERTNTVCRCRCPDGFPS 130
Db      111 EMVADCSATSDRKCQRTGLYY-----YDKF-----PESCRPTCKCQ---- 149
QY      131 NETSSKAPCRKHTNCVFGLLLTQKNATHDNICSGNSESTQKVDKTHTCPPCAPPELLG 190
Db      150 -----GIPVLQECNSTANTVC---SSSVSNVD-THTCPPCAPPELLG 187
QY      191 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVSHEDPEVHNNAKTKPREOY 250
Db      188 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWVDGVSHEDPEVHNNAKTKPREOY 247
QY      251 NSTYRVSVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRD 310
Db      248 NSTYRVSVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRD 307
QY      311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 370
Db      308 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 367
QY      371 WOQGNVFCSCVMHEALHNYTKQSLSLSPG 400
Db      368 WOQGNVFCSCVMHEALHNYTKQSLSLSPG 397

RESULT 8
US-09-097-827-11
; Sequence 11, Application US/08097827
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
;               Goodwin, Ray
;               Fanslow, William
;               Gayle, Richard
; TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
;               OK40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/097,827
; APPLICATION DATA:
; FILING DATE: 23-Jul-1993
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-097-827-11

Query Match          59.5%; Score 1332; DB 1; Length 438;
Best Local Similarity 62.4%; Pred. No. 1.2e-103;
Matches 262; Conservative 23; Mismatches 75; Indels 60; Gaps 6;

QY 20 CDKCPGTYLKQCTAKWKTVCAPCPDHYTD--SMHTSDECLYCSVPCKELQYVQECN 77
DB 39 CRECPQGHGMVNRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNH--RSGSELQNCT 96
QY 78 RTHNRVCECKEGRYLEIEFLCKHRSCPPGFGVVQAGTPERTVCKRCPPDGFFSNETSSKA 137
DB 97 PTQDTVCRCR-----PGTQPRQDSGYKLGVDVCPVCPGHFS--PCNNQ 137
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----EST----- 171
DB 138 ACKPWNTCLSGKQTRHPASDSLDVAVCEDRSLLATLLWETQRTPTTQSTTVMPTRS 197
QY 172 -----QKVDKTHTCPPCAPPELLGSPVFLPPPKDQTLMSRTPETVTCVVVDV 220
DB 198 ELPSTPLVPRSCDKTHTCPPCAPPAEAGAPSVFLPPPKDQTLMSRTPETVTCVVVDV 257
QY 221 SHEDPEVKFNWYDGVVEVHNATKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNK 280
DB 258 SHEDPEVKFNWYDGVVEVHNATKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNK 317
QY 281 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 340
DB 318 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 377
QY 341 PENNYKTTTPVLDSGDFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
DB 378 PENNYKTTTPVLDSGDFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 437

RESULT 9
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Farnlow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
; TITLE OF INVENTION: OK40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
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RESULT 11  
 US-08-484-438-10  
 ; Sequence 10, Application US/08484438  
 ; Patent No. 5811098  
 ; Patent No. 5811098 5780031  
 ;  
 GENERAL INFORMATION:  
 APPLICANT: Plowman, Gregory D.  
 APPLICANT: Culouscou, Jean-Michel  
 APPLICANT: Shoyab, Mohammed  
 APPLICANT: Siegall, Clay B.  
 APPLICANT: Hellstr m, Ingegerd  
 APPLICANT: Hellstr m, Karl E.  
 TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484,438  
 FILING DATE: 07-JUN-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 530  
 CLASSIFICATION: 530  
 FILING DATE: 14-OCT-1994  
 APPLICATION NUMBER: US 08/150,704  
 FILING DATE: 10-NOV-1993  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/981,165

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RESULT 12
US-09-590-656-2
; Sequence 2, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

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; LENGTH: 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-2

Query Match
  55.9%; Score 1252; DB 4; Length 704;
Best Local Similarity 57.8%; Pred. No. 1.2e-96;
Matches 275; Conservative 20; Mismatches 69; Indels 112; Gaps 16;

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Db 242 CPPGFMGRTCEKACELHTFGRTCKERCSCGQBGCKSYVFCCLPDP---YGCSCATGWKGLQC 298
Qy 63 SPVCKELOY---VKQECNRTHNRVCECKEGRYLEIEFCLKXRSRCPGFGVQA---GTPE 116
Db 299 NEACHPGFGYGPDCCKLRCSNNGEMCDRFOG-----CL-----CSPGWQGLQCEGIPR 347
Qy 117 R-----NTVCKRC-----PDG-----FGL---LLTQKQNA-----THDNICSGNSES 170
Db 348 MTPKIVDLDPDHIEVNSGKFNPKCKASGWPLPTNEEMTLVKPDGTGLVLPKDFNHTDHSVA 407
Qy 138 PCRKHT-----NCSV-----FGL---LLTQKQNA-----THDNICSGNSES 170
Db 408 IFTIHRILPPDGSVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVDTGHNFAVINISS 467
Qy 171 -----TQKVDKTHTCPPCPAPPELLGGPSVFLPPPKKDTLMISRTPETVTCVVVDVSHED 224
Db 468 EYFGEKPKSCDKTHTCPPCPAPPELLGGPSVFLPPPKKDTLMISRTPETVTCVVVDVSHED 527
Qy 225 PEVKFNWYDGVGVHNAKTPREEQYNSTRVSVVSVLTVLHODWLNKGEYKCKVSNKALPA 284
Db 528 PEVKFNWYDGVGVHNAKTPREEQYNSTRVSVVSVLTVLHODWLNKGEYKCKVSNKALPA 587
Qy 285 PIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENN 344
Db 588 PIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENN 647
Qy 345 YKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 400
Db 648 YKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPG 703

RESULT 14
US-08-957-063-16
; Sequence 16, Application US/08957063
; Patent No. 6025157
; GENERAL INFORMATION:
; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
; TITLE OF INVENTION: Neurturin Receptor
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,063
; FILING DATE: 24-Oct-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/871
; FILING DATE: 9-Jun-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 913
; FILING DATE: 18-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1086P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 664 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-957-063-16

Query Match
  55.8%; Score 1249.5; DB 3; Length 664;
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Search completed: March 8, 2005, 14:48:11  
Job time : 23.8688 secs

## RESULT 15

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 60.4374 Seconds  
(without alignments)  
2177.757 Million cell updates/sec

Title: US-09-389-782a-5  
Perfect score: 2240  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2240	100.0	400	10	US-09-389-782-5
2	2227	99.4	406	10	US-09-389-782-6
3	2225	99.3	425	16	US-10-467-243-20
4	2222.5	99.0	407	10	US-09-389-782-3
5	2218.5	99.0	413	10	US-09-389-782-4
6	2191	97.8	404	10	US-09-389-782-7
7	1522.5	68.0	659	14	US-10-363-427-12
8	1517	67.7	467	17	US-10-901-735-4
9	1514.5	67.6	490	14	US-10-363-427-4
10	1514.5	67.6	720	14	US-10-363-427-8
11	1502	67.1	518	14	US-10-313-852-1
12	1502	67.1	518	14	US-10-313-852-3
13	1502	67.1	518	14	US-10-314-033-1
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					Sequence 6, Appli
					Sequence 20, Appli
					Sequence 3, Appli
					Sequence 4, Appli
					Sequence 7, Appli
					Sequence 12, Appli
					Sequence 4, Appli
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 3, Appli

14	1502	67.1	518	14	US-10-314-033-3	Sequence 3, Appli
15	1502	67.1	518	15	US-10-423-507-1	Sequence 1, Appli
16	1461.5	65.2	443	14	US-10-151-071-5	Sequence 5, Appli
17	1461.5	65.2	443	14	US-10-166-232A-5	Sequence 5, Appli
18	1459.5	65.2	444	16	US-10-467-243-24	Sequence 24, Appli
19	1392.5	62.2	608	14	US-10-363-427-10	Sequence 10, Appli
20	1384.5	61.8	444	14	US-10-363-427-2	Sequence 2, Appli
21	1384.5	61.8	628	14	US-10-363-427-6	Sequence 6, Appli
22	1352	60.4	360	9	US-09-949-713-11	Sequence 11, Appli
23	1352	60.4	376	9	US-09-949-713-22	Sequence 22, Appli
24	1352	60.4	376	14	US-10-084-139-10	Sequence 10, Appli
25	1350.5	60.3	396	14	US-10-193-616-14	Sequence 14, Appli
26	1345.5	60.1	398	15	US-10-622-407-14	Sequence 14, Appli
27	1283.5	57.3	380	9	US-09-948-018-39	Sequence 39, Appli
28	1280	57.1	446	9	US-09-792-2008-10	Sequence 10, Appli
29	1273	56.8	404	9	US-09-948-018-16	Sequence 16, Appli
30	1267	56.6	360	15	US-10-390-566-20	Sequence 20, Appli
31	1267	56.6	360	15	US-10-390-566-27	Sequence 27, Appli
32	1267	56.6	367	15	US-10-390-566-19	Sequence 19, Appli
33	1267	56.6	367	15	US-10-390-566-26	Sequence 26, Appli
34	1266	56.5	360	15	US-10-390-566-7	Sequence 7, Appli
35	1266	56.5	360	15	US-10-390-566-14	Sequence 14, Appli
36	1266	56.5	367	15	US-10-390-566-6	Sequence 6, Appli
37	1266	56.5	367	15	US-10-390-566-13	Sequence 13, Appli
38	1264	56.4	542	9	US-09-792-2008-16	Sequence 16, Appli
39	1257	56.1	380	9	US-09-948-018-36	Sequence 36, Appli
40	1257	56.1	404	15	US-10-258-368-15	Sequence 15, Appli
41	1256	56.1	334	15	US-10-258-368-8	Sequence 8, Appli
42	1256	56.1	366	15	US-10-258-368-6	Sequence 6, Appli
43	1254.5	56.0	810	14	US-10-232-838-15	Sequence 15, Appli
44	1254.5	56.0	934	14	US-10-232-838-17	Sequence 17, Appli
45	1254.5	56.0	949	14	US-10-232-838-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1  
US-09-389-782-5  
; Sequence 5, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-5

Query Match	100.0%	Score 2240;	DB 10;	Length 400;
Best Local Similarity	100.0%	Pred. No. 4.2e-141;		
Matches 400;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	61	YCSVPCKELOYKQCNTR	THRVCSCKGRYLEIFCL	KHRSCTPGFGVVGAGTPTNTV 120
QY	121	CKRCPDGFFSNETSSK	APCRKHTNCSVFGLLLT	TQGNATHDNCNSESSTQKVDKHTC 180
DB	121	CKRCPDGFFSNETSSK	APCRKHTNCSVFGLLLT	TQGNATHDNCNSESSTQKVDKHTC 180

QY 181 PPCPAPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHN 240  
Db 181 PPCPAPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHN 240  
QY 241 AKTKPREOYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAKGQPREP 300  
Db 241 AKTKPREOYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAKGQPREP 300  
QY 301 QVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPENNYKTTTPVLDSDGSFFL 360  
Db 301 QVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPENNYKTTTPVLDSDGSFFL 360  
QY 361 YSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 400  
Db 361 YSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 400

RESULT 2  
US-09-389-782-6  
; Sequence 6, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Maxygen Holdings Ltd.  
; APPLICANT: Haaning, Jesper Mortensen  
; APPLICANT: Halkier, Torben  
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES  
; FILE REFERENCE: 0226w0310  
; CURRENT APPLICATION NUMBER: US/10/467,243  
; CURRENT FILING DATE: 2003-08-06  
; PRIOR APPLICATION NUMBER: DK PA 2001 00214  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/267,843  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: DK PA 2001 00498  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 60/278,320  
; PRIOR FILING DATE: 2001-03-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19  
US-10-467-243-20

Query Match 99.4%; Score 2227; DB 10; Length 406;  
Best Local Similarity 98.5%; Pred. No. 3.1e-140;  
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;  
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Db 1 ETTPPKYLHYDEETSHQLLCKDCKPPGYLKHQCTAKWTVCAPCPDHYTDSWHTSDECL 60  
QY 61 YCSPVCKELQYVKECNRNTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERNTV 120  
Db 61 YCSPVCKELQYVKECNRNTHNRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPERNTV 120  
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGSESTOK-----V 174  
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QY 175 DKHTHTCPAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234  
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QY 235 GVEVHNKTKPREEQYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAK 294  
Db 235 GVEVHNKTKPREEQYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAK 294  
QY 241 GVEVHNKTKPREEQYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAK 300  
Db 241 GVEVHNKTKPREEQYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAK 300  
QY 295 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPENNYKTTTPVLDSD 354  
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QY 301 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPENNYKTTTPVLDSD 360  
Db 301 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPENNYKTTTPVLDSD 360  
QY 355 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 400  
Db 355 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 400

RESULT 3  
US-10-467-243-20  
; Sequence 20, Application US/10467243

Publication No. US20040132971A1  
GENERAL INFORMATION:  
APPLICANT: Maxygen Holdings Ltd.  
APPLICANT: Haaning, Jesper Mortensen  
APPLICANT: Halkier, Torben  
TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES  
FILE REFERENCE: 0226w0310  
CURRENT APPLICATION NUMBER: US/10/467,243  
CURRENT FILING DATE: 2003-08-06  
PRIOR APPLICATION NUMBER: DK PA 2001 00214  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/267,843  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: DK PA 2001 00498  
PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: US 60/278,320  
PRIOR FILING DATE: 2001-03-23  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 425  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19  
US-10-467-243-20

Query Match 99.3%; Score 2225; DB 16; Length 425;  
Best Local Similarity 98.8%; Pred. No. 4.5e-140;  
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Db 22 ETTPPKYLHYDEETSHQLLCKDCKPPGYLKHQCTAKWTVCAPCPDHYTDSWHTSDECL 81  
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QY 177 THTCPPCPAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 236  
Db 202 THTCPPCPAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 261  
QY 237 EVHNKTKPREEQYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAKGQ 296  
Db 262 EVHNKTKPREEQYNSTRVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAKGQ 321  
QY 297 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPENNYKTTTPVLDSDG 356  
Db 322 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVWESNGOPENNYKTTTPVLDSDG 381  
QY 357 SFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 400  
Db 382 SFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 425

RESULT 4  
US-09-389-782-3  
; Sequence 3, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match      99.2%; Score 2222.5; DB 10; Length 407;
Best Local Similarity 98.0%; Pred. No. 6.3e-140;
Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60
Db      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60

Qy      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120
Db      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120

Qy      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKV----- 174
Db      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKAAABPKS 180

Qy      175  -DKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENMYV 233
Db      181  CDKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENMYV 240

Qy      234  DGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 293
Db      241  DGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 300

Qy      294  KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 353
Db      301  KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 360

Qy      354  SDGSFELYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
Db      361  SDGSFELYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 407

RESULT 5
US-09-389-782-4
; Sequence 4, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-4

Query Match      99.0%; Score 2218.5; DB 10; Length 413;
Best Local Similarity 96.6%; Pred. No. 1.2e-139;
Matches 399; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

Qy      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60
Db      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60

Qy      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120
Db      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120

Qy      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK----- 173
Db      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK----- 173

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match      99.2%; Score 2222.5; DB 10; Length 407;
Best Local Similarity 98.0%; Pred. No. 6.3e-140;
Matches 399; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

Qy      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60
Db      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60

Qy      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120
Db      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120

Qy      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKV----- 174
Db      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKAAABPKS 180

Qy      175  -DKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENMYV 233
Db      181  CDKTHTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENMYV 240

Qy      234  DGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 293
Db      241  DGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 300

Qy      294  KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 353
Db      301  KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 360

Qy      354  SDGSFELYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
Db      361  SDGSFELYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 407

RESULT 6
US-09-389-782-7
; Sequence 7, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-7

Query Match      97.8%; Score 2191; DB 10; Length 404;
Best Local Similarity 97.8%; Pred. No. 7.7e-138;
Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

Qy      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60
Db      1  ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCDPDHYTDSWHTSDECL 60

Qy      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120
Db      61  YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTNV 120

Qy      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKV---DK 176
Db      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGG 180

Qy      177  THTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENMYVDGV 236
Db      181  GGTCPPCAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENMYVDGV 240

Qy      237  EVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 296
Db      241  EVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 300

Qy      297  PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDG 356
Db      301  PREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDG 360

Qy      357  SFELYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
Db      361  SFELYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404
```

## RESULT 7

US-10-363-427-12  
; Sequence 12, Application US/10363427  
; Publication No. US20030195338A1  
; GENERAL INFORMATION:  
; APPLICANT: MedExGen, Inc.  
; APPLICANT: CHUNG, Yong Hoon  
; APPLICANT: HAN, Ji Woong  
; APPLICANT: LEE, Hye Ja  
; APPLICANT: CHOI, Eun Yong  
; APPLICANT: KIM, Jin Mi  
; APPLICANT: YIM, Soo Bin  
; TITLE OF INVENTION: Concatametric Immunoadhesion  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/363,427  
; CURRENT FILING DATE: 2003-02-28  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 12  
; LENGTH: 659  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-363-427-12

Query Match 68.0%; Score 1522.5; DB 14; Length 659;  
Best Local Similarity 65.4%; Pred. No. 4e-93;  
Matches 295; Conservative 16; Mismatches 75; Indels 65; Gaps 5;  
QY 9 HYDEETSHQLCDKCPPTGTYLKQHCTAKWKTVCAPCPDHYHYTDSWHTSDCLYCSFVCKE 68  
Db 214 YYDQ--TAQMCCKSCSPGQAHKVFCTKTSITVDCSDCEDSTYTQLMNNVPECLSGRCSS 271  
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHSRCPGPGVVGAGTPTERTVCK 122  
Db 272 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVCK 331  
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQGNATHDNIC----- 164  
Db 332 PCAPGTFTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 387  
QY 165 --SGNSSTQ-----KVDKTHTCPPCPAPPELL 189  
Db 388 PVSTRSQHTQTPPTSTAPSTSFLLPMGSPPAEGSTGDAEPKSCDKTHTCCPAPPELL 447  
QY 190 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 249  
Db 448 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 507  
QY 250 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309  
Db 508 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 567  
QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 369  
Db 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 627  
QY 370 RWQGNVFCSCVMHEALHNNHYTKSLSLSPG 400  
Db 628 RWQGNVFCSCVMHEALHNNHYTKSLSLSPG 658

## RESULT 8

US-10-901-735-4  
; Sequence 4, Application US/10901735  
; Publication No. US20050032183A1  
; GENERAL INFORMATION:  
; APPLICANT: AMGEN, Inc.  
; APPLICANT: OSSUND, Timothy D.  
; APPLICANT: CLOSTON, Christi  
; APPLICANT: CRAMPTON, Shon  
; APPLICANT: BASS, Randal  
; TITLE OF INVENTION: CRYSTALLINE POLYPEPTIDES  
; FILE REFERENCE: A-859

; CURRENT APPLICATION NUMBER: US/10/901,735  
; CURRENT FILING DATE: 2004-07-29  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion polypeptide  
US-10-901-735-4

Query Match 67.7%; Score 1517; DB 17; Length 467;  
Best Local Similarity 64.4%; Pred. No. 6.3e-93;  
Matches 290; Conservative 20; Mismatches 76; Indels 64; Gaps 4;  
QY 9 HYDEETSHQLCDKCPPTGTYLKQHCTAKWKTVCAPCPDHYHYTDSWHTSDCLYCSFVCKE 68  
Db 23 YYDQ--TAQMCCKSCSPGQAHKVFCTKTSITVDCSDCEDSTYTQLMNNVPECLSGRCSS 80  
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHSRCPGPGVVGAGTPTERTVCK 122  
Db 81 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVCK 140  
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNS----- 168  
Db 141 PCAPGTFTNTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTPTSRMAPGAVHLPQ 196  
QY 169 -----ESTQKVDKTHTCPPCPAPPELLG 190  
Db 197 PVSTRSQHTQTPPTSTAPSTSFLLPMGSPPAEGSTGDAEPKSCDKTHTCCPAPPELLG 256  
QY 191 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 250  
Db 257 GGSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQ 316  
QY 251 NSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 310  
Db 317 NSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 376  
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 370  
Db 377 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 436  
QY 371 WQGNVFCSCVMHEALHNNHYTKSLSLSPG 400  
Db 437 WQGNVFCSCVMHEALHNNHYTKSLSLSPG 466

## RESULT 9

US-10-363-427-4  
; Sequence 4, Application US/10363427  
; Publication No. US20030195338A1  
; GENERAL INFORMATION:  
; APPLICANT: MedExGen, Inc.  
; APPLICANT: CHUNG, Yong Hoon  
; APPLICANT: HAN, Ji Woong  
; APPLICANT: LEE, Hye Ja  
; APPLICANT: CHOI, Eun Yong  
; APPLICANT: KIM, Jin Mi  
; APPLICANT: YIM, Soo Bin  
; TITLE OF INVENTION: Concatametric Immunoadhesion  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/363,427  
; CURRENT FILING DATE: 2003-02-28  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 4  
; LENGTH: 490  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-363-427-4

```
Query Match      67.6%; Score 1514.5; DB 14; Length 490;
Best Local Similarity 65.2%; Pred. No. 9.8e-93;
Matches 294; Conservative 16; Mismatches 76; Indels 65; Gaps 5;

QY 9 HYDETSQHLCDKCPGTYLKHCTAKWTKVACPCPDHYVTDSDWHTSDCLYCSPVCKE 68
DB 45 YYDQ--TAQWCCSKCSGQAKVFCYKTSYTDVCDSCEDSTYTLQWNVPECLSGSRCS 102
QY 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPERNTVCK 122
DB 103 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARPGTETSDVCK 162
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
DB 163 PCAPGTFSNTSSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 218
QY 165 --SGNSESTQ-----KVDKTHTCPPCPAPELL 189
DB 219 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPPAEGSTGDAEPKSCDKTHTCCPCPAPELL 278
QY 190 GSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 249
DB 279 GSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 338
QY 250 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309
DB 339 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 398
QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKS 369
DB 399 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKS 458
QY 370 RWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
DB 459 RWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 489

RESULT 10
US-10-363-427-8
; Sequence 8, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MedGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 8
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-8

Query Match      67.6%; Score 1514.5; DB 14; Length 720;
Best Local Similarity 65.2%; Pred. No. 1.5e-92;
Matches 294; Conservative 16; Mismatches 76; Indels 65; Gaps 5;

QY 9 HYDETSQHLCDKCPGTYLKHCTAKWTKVACPCPDHYVTDSDWHTSDCLYCSPVCKE 68
DB 275 YYDQ--TAQWCCSKCSGQAKVFCYKTSYTDVCDSCEDSTYTLQWNVPECLSGSRCS 332
QY 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPERNTVCK 122
DB 333 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARPGTETSDVCK 392
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QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC----- 164
DB 393 PCAPGTFSNTSSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 448
QY 165 --SGNSESTQ-----KVDKTHTCPPCPAPELL 189
DB 449 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPPAEGSTGDAEPKSCDKTHTCCPCPAPELL 508
QY 190 GSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 249
DB 509 GSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 568
QY 250 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 309
DB 569 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 628
QY 310 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKS 369
DB 629 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKS 688
QY 370 RWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 400
DB 689 RWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 719

RESULT 11
US-10-313-852-1
; Sequence 1, Application US/10313852
; Publication No. US20030103942A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 22627200420
; CURRENT APPLICATION NUMBER: US/10/313,852
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-1

Query Match      67.1%; Score 1502; DB 14; Length 518;
Best Local Similarity 63.8%; Pred. No. 7.1e-92;
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;

QY 9 HYDETSQHLCDKCPGTYLKHCTAKWTKVACPCPDHYVTDSDWHTSDCLYCSPVCKE 68
DB 74 YYDQ--TAQWCCSKCSGQAKVFCYKTSYTDVCDSCEDSTYTLQWNVPECLSGSRCS 131
QY 69 LQYVQECNTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPERNTVCK 122
DB 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARPGTETSDVCK 191
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS----- 168
DB 192 PCAPGTFSNTSSTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
QY 169 -----ESTQKVDKTHTCPPCPAPELL 190
DB 248 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPPAEGSTGDEPKSCDKTHTCCPCPAPELL 307
QY 191 GSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 250
DB 308 GSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 367
```

QY 251 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSRD 310  
Db 368 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPMQKTIISKAKGPREPOVYTLPPSRD 427  
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 370  
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487  
QY 371 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 400  
Db 488 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 517  
RESULT 12  
US-10-313-852-3  
; Sequence 3, Application US/10313852  
; Publication No. US20030103942A1  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING  
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED  
; FILE REFERENCE: 226272004420  
; CURRENT APPLICATION NUMBER: US/10/313,852  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-313-852-3  
Query Match 67.1%; Score 1502; DB 14; Length 518;  
Best Local Similarity 63.8%; Pred. No. 7,1e-92;  
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;  
QY 9 HYDEETSHQLLCKCPGGTYLKQCTAKWKVCAPCPDHYHDTSDWHTSDECLYCSVPCKE 68  
Db 74 YDQ--TAQCCSKCSPGQAHKVFCTSDTCDSCEDSTYTQLMNNWPECLSCGRCSS 131  
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFLCKHRSCPPGFGVVOAGTPERTVCK 122  
Db 132 DVETQACTREONRICTCRPGWYCALSKQECRLCAPLRCRPGFGVARGTETSDVCK 191  
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----168  
Db 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247  
QY 169 -----ESTQKVDKTHTCPCPAPELLG 190  
Db 248 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPSPABSGTGDEPKSCDKTHTCPCPAPELLG 307  
QY 191 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 250  
Db 308 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 367  
QY 251 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSRD 310  
Db 368 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPMQKTIISKAKGPREPOVYTLPPSRD 427  
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 370  
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487  
QY 371 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 400  
Db 488 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 517  
RESULT 14  
US-10-314-033-3  
; Sequence 3, Application US/10314033  
; Publication No. US20030113295A1  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

Db 488 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 517  
RESULT 13  
US-10-314-033-1  
; Sequence 1, Application US/10314033  
; Publication No. US20030113295A1  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING  
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED  
; FILE REFERENCE: 226272004420  
; CURRENT APPLICATION NUMBER: US/10/314,033  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-314-033-1  
Query Match 67.1%; Score 1502; DB 14; Length 518;  
Best Local Similarity 63.8%; Pred. No. 7,1e-92;  
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;  
QY 9 HYDEETSHQLLCKCPGGTYLKQCTAKWKVCAPCPDHYHDTSDWHTSDECLYCSVPCKE 68  
Db 74 YDQ--TAQCCSKCSPGQAHKVFCTSDTCDSCEDSTYTQLMNNWPECLSCGRCSS 131  
QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFLCKHRSCPPGFGVVOAGTPERTVCK 122  
Db 132 DVETQACTREONRICTCRPGWYCALSKQECRLCAPLRCRPGFGVARGTETSDVCK 191  
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----168  
Db 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247  
QY 169 -----ESTQKVDKTHTCPCPAPELLG 190  
Db 248 PVSTRSQHTQTPPEPSTAPSTSFLLPMGPPSPABSGTGDEPKSCDKTHTCPCPAPELLG 307  
QY 191 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 250  
Db 308 GPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 367  
QY 251 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSRD 310  
Db 368 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPMQKTIISKAKGPREPOVYTLPPSRD 427  
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 370  
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487  
QY 371 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 400  
Db 488 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 517  
RESULT 14  
US-10-314-033-3  
; Sequence 3, Application US/10314033  
; Publication No. US20030113295A1  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

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; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-314-033-3

Query Match 67.1%; Score 1502; DB 14; Length 518;
Best Local Similarity 63.8%; Pred. No. 7.1e-92;
Matches 287; Conservative 21; Mismatches 78; Indels 64; Gaps 4;

QY 9 HYDEETSHQLLCKPCPGTYLKQHTAKWTKVACPCPDHYTDSWHTSDRECLYCSVPVCKE 68
DB 74 YYDQ--TAQMCCKSKSPGQAKVFTKTSITVCDSCEDSTYTLQNMWVPECLSCGRCS 131
QY 69 LQYVQECNRTNHRVCEKGRYLEI-----EFCLKHRSCEPGFGVQAGTPTERTVCK 122
DB 132 DQVETOACTREONRICTCRPGWYCALSKQEGCRCLCAPLRKCRPGFGVARGTETSDVVK 191
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS-----168
DB 192 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSTPTRSMAPGAVHLPQ 247
QY 169 -----ESTQKVDKHTHTCCPPCAPPELLG 190
DB 248 PVSTRSQHTOPTPEPSTAPSTFLLPMGPPSPPAEGSTGDEPKSCDKHTHTCCPPCAPPELLG 307
QY 191 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNNAKTKPREEQ 250
DB 308 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNNAKTKPREEQ 367
QY 251 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRD 310
DB 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRD 427
QY 311 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 370
DB 428 ELTKNQVSLTCLVKGFYPRHIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSR 487
QY 371 WQGNVFSCVMHEALHNHYTQKSLSLSPG 400
DB 488 WQGNVFSCVMHEALHNHYTQKSLSLSPG 517

Search completed: March 8, 2005, 15:16:03
Job time : 62.4374 secs
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## RESULT 15

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US-10-423-507-1
; Sequence 1, Application US/10423507
; Publication No. US20030219735A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Barrie, J.
; TITLE OF INVENTION: METABOLICALLY ACTIVATED RECOMBINANT
; VIRAL VECTORS AND METHODS FOR THEIR PREPARATION AND USE
; FILE REFERENCE: 226272004302
; CURRENT APPLICATION NUMBER: US/10/423,507
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 09/634,126
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 60/160,080
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.3022 Seconds  
(without alignments)  
2360.831 Million cell updates/sec

Title: US-09-389-782a-5  
Perfect score: 2240  
Sequence: 1 ETFPKVLHYDETSQLLC.....VMHEALNHVYTKSLSPG 400  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	55.1	330	1 GHU	Ig gamma-1 chain C
2	1229	54.9	255	4 S31866	Ig gamma-1 chain C
3	1225	54.7	374	2 S69339	Ig heavy chain V x
4	1183.5	52.8	234	2 PT0307	Ig gamma chain C x
5	1154.5	51.5	377	2 A23111	Ig gamma-3 chain C
6	1152.5	51.5	377	2 A60764	Ig gamma-3 chain C
7	1148.5	51.3	326	1 G2HU	Ig gamma-2 chain C
8	1136	50.7	327	1 G4HU	Ig gamma-4 chain C
9	1133.5	50.6	289	1 G3HUI	Ig gamma-3 heavy c
10	923	41.2	323	1 GHRB	Ig gamma chain C x
11	917.5	41.0	328	2 I47160	Ig gamma 2b chain
12	917.5	41.0	328	2 I47159	Ig gamma 2a chain
13	915.5	40.9	277	2 I47162	Ig gamma 4 chain C
14	904.5	40.4	329	1 G2GP	Ig gamma-2 chain C
15	895.5	40.0	328	2 I47158	Ig gamma-1 chain c
16	889.5	39.7	328	2 I47161	Ig gamma 3 chain c
17	861.5	38.5	470	2 S22080	Ig heavy chain pre
18	851.5	38.0	308	2 S30554	Ig heavy chain C x
19	851.5	38.0	472	2 S31459	Ig gamma-1 chain -
20	847.5	37.8	329	1 G3MSC	Ig gamma-3 chain C
21	843	37.6	333	2 PS0018	Ig gamma-2b chain
22	841.5	37.6	338	1 G3MSM	Ig gamma-3 chain C
23	830	37.1	444	2 FC4436	monoclonal antibod
24	820	36.6	324	1 G1MS	Ig gamma-1 chain C
25	820	36.6	326	2 PS0017	Ig gamma-1 chain C
26	820	36.6	393	1 G1MSM	Ig gamma-1 chain C
27	812.5	36.3	330	1 G2MSA	Ig gamma-2a chain
28	812.5	36.3	339	1 G2MSAM	Ig gamma-2a chain
29	812.5	36.3	469	2 S37483	Ig gamma-2a chain

RESULT 1  
GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004

C;Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: UNIPROT:P01857; EMBL:Z17370

A;Note: this sequence has the Gln(17) alleotypic marker, 97-Lys, and the Gln(1) markers, 2

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a s

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96, 'R', 98-135 <CUN>

A;Note: this sequence has the Gln(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,

A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),









F:20-82/Domain: immunoglobulin homology <IM1>  
F:130-199/Domain: immunoglobulin homology <IM2>  
F:236-303/Domain: immunoglobulin homology <IM3>  
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.2%; Score 923; DB 1; Length 323;  
Best Local Similarity 61.5%; Pred. No. 4.8e-49;  
Matches 177; Conservative 33; Mismatches 46; Indels 32; Gaps 5;  
QY 123 RCPDGFSS-----NETSKAPCRKHTNCSVFGLLLTQGNATHDNCISGSESTOKVDKT 177  
DB 57 RQSSGLYSLSVSVTSQP-----VTCNV-----AHPATTKVDKT 94  
QY 178 ---HTC---PPCAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 232  
DB 95 VAPSTCSKPTCPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSDDDPEVQFTWY 154  
QY 233 YDGVVEVNAKTPREEQNSTYRVSVLTQVHQLWNGKEYCKVSKVSKALPAPIETKIS 291  
DB 155 INNEQVTRAPPLRKEQNFSTIRVSVLTPIHQDWLNGKEYCKVSKVSKALPAPIETKIS 214  
QY 293 AKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEFESGVNGPENNYKTTTPVVL 352  
DB 215 ARGQPLEPKVYTMGPREELSRSVSLTCMINGFYPSDISEVEKKGKAEADNTKTPAVL 274  
QY 353 DSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400  
DB 275 DSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 322

## RESULT 11

I47160  
Ig gamma 2b chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126  
C:Genetics:  
A:Gene: IgG2b  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 41.0%; Score 917.5; DB 2; Length 328;  
Best Local Similarity 60.5%; Pred. No. 1.1e-48;  
Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;  
QY 125 PDGFFNETSSKAPC-----RKHTNCSVFGLLLTQGNATHDNCISGSESTOKVDK--T 177  
DB 59 PSLGLYSLSMVTVPASSLSKSYTCNV-----NHPATTTKVDKRVGT 100  
QY 178 HTCPPCP-----APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 231  
DB 101 KTKPPCIPACESP-----GPSVFIFPPPKPKDTLMISRTPTQVTCVVVDVSDQENPEVQFSW 156  
QY 232 YDGVVEVNAKTPREEQNSTYRVSVLTQVHQLWNGKEYCKVSKVSKALPAPIETKIS 291  
DB 157 YDGVVEVHTAQRPEEQNSTYRVSVLPIHQDWLNGKEYCKVSKVSKALPAPIETKIS 216  
QY 292 KAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEFESGVNGQ--PENNYKTTTP 349  
DB 217 KAKGQTRPQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQGNQPEPEGNRYRTTP 276  
QY 350 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400  
DB 277 PQDDVDGTYFLYSKFSDVKASWQGGIFQCAVMHEALHNHYTQKSISKTPG 327

## RESULT 12

I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124  
C:Genetics:  
A:Gene: IgG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 41.0%; Score 917.5; DB 2; Length 328;  
Best Local Similarity 60.5%; Pred. No. 1.1e-48;  
Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;  
QY 125 PDGFFNETSSKAPC-----RKHTNCSVFGLLLTQGNATHDNCISGSESTOKVDK--T 177  
DB 59 PSLGLYSLSMVTVPASSLSKSYTCNV-----NHPATTTKVDKRVGT 100  
QY 178 HTCPPCP-----APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 231  
DB 101 KTKPPCIPACESP-----GPSVFIFPPPKPKDTLMISRTPTQVTCVVVDVSDQENPEVQFSW 156  
QY 232 YDGVVEVNAKTPREEQNSTYRVSVLTQVHQLWNGKEYCKVSKVSKALPAPIETKIS 291  
DB 157 YDGVVEVHTAQRPEEQNSTYRVSVLPIHQDWLNGKEYCKVSKVSKALPAPIETKIS 216  
QY 292 KAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEFESGVNGQ--PENNYKTTTP 349  
DB 217 KAKGQTRPQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQGNQPEPEGNRYRTTP 276  
QY 350 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400  
DB 277 PQDDVDGTYFLYSKFSDVKASWQGGIFQCAVMHEALHNHYTQKSISKTPG 327

## RESULT 13

I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47162  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47162  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <KAC>  
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130  
C:Genetics:  
A:Gene: IgG4  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:82-151/Domain: immunoglobulin homology <IM>

Query Match 40.9%; Score 915.5; DB 2; Length 277;  
Best Local Similarity 61.3%; Pred. No. 1.2e-48;  
Matches 176; Conservative 34; Mismatches 48; Indels 29; Gaps 6;  
QY 125 PDGFFNETSSKAPC-----RKHTNCSVFGLLLTQGNATHDNCISGSESTOKVDK--T 177  
DB 59 PSLGLYSLSMVTVPASSLSKSYTCNV-----NHPATTTKVDKRVGT 100  
QY 178 HTCPPCP-----APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 231  
DB 101 KTKPPCIPACESP-----GPSVFIFPPPKPKDTLMISRTPTQVTCVVVDVSDQENPEVQFSW 156  
QY 232 YDGVVEVNAKTPREEQNSTYRVSVLTQVHQLWNGKEYCKVSKVSKALPAPIETKIS 291  
DB 157 YDGVVEVHTAQRPEEQNSTYRVSVLPIHQDWLNGKEYCKVSKVSKALPAPIETKIS 216  
QY 292 KAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEFESGVNGQ--PENNYKTTTP 349  
DB 217 KAKGQTRPQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQGNQPEPEGNRYRTTP 276  
QY 350 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 400  
DB 277 PQDDVDGTYFLYSKFSDVKASWQGGIFQCAVMHEALHNHYTQKSISKTPG 327

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F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Diulfide bonds: #status experimental
F;142-202/Diulfide bonds: #status experimental
F;178/Binding site: carbonydrate (Aen) (covalent) #status experimental
F;248-308/Diulfide bonds: #status experimental

Query Match 40.4%; Score 904.5; DB 1; Length 329;
Best Local Similarity 60.3%; Pred. No. 6.5e-48;
Matches 173; Conservative 30; Mismatches 53; Indels 31; Gaps 3;

QY 127 GFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSBSTOKVDKT----- 177
DB 61 GLYSLSMTVTVPSSQKATCNV-----AHPASSTKVDKVTPIPTPZP 102

QY 178 --HTCCPPCAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDG 235
DB 103 BPCTCPKCPPENLGGPSVFLPPPKPKDTLMISLTPTVTCVVVDVSDPEVQTFWFDN 162

QY 236 VEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKG 295
DB 163 KPVGNAETKPRVEQYNTTFRVESVLPIQHQDWLGRGEFKCKVYNKALPAPIETKISKTKG 222

QY 296 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTTTPVLD 353
DB 223 APRMPDVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTTTPVLD 282

QY 354 SDGSFFLYSKLTVDKSRWQGNVFCSSVMHEALHNHYTKSLSLSPG 400
DB 283 ADGSFFLYSKLTVDKSAWQGVYTCSSVMHEALHNHYTKAISRSPG 329

RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J. E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <EAC>
A;Cross-references: EMBL:U03778; NID:G433121; PIDN:AAA52216.1; PID:G433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 895.5; DB 2; Length 328;
Best Local Similarity 60.4%; Pred. No. 2.3e-47;
Matches 174; Conservative 32; Mismatches 51; Indels 31; Gaps 5;

QY 125 PDGFFNETSSKAPC---RKHTNCSVFGLLLTQKGNATHDNICSGNSBSTOKVDK--- 176
DB 59 PSLGLSLSMTVTVPASSLSKSKYTCNV-----NHPATTTKVDKRVGI 100

QY 177 --THTCCPPCAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 234
DB 101 HQPOTCFPCGCE-VAGPSVFIFPPPKPKDTLMISQPEVTCVVVDVSDPEVQTFWFDN 159

QY 235 GUEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAK 294
DB 160 GUEVHTAETPRKEEQNSTYRVVSVLPIQHQDWLKGKBFKCKVYNVLDLPAPITRTISKAI 219

QY 295 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPVLD 352
DB 220 GQSRBQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPVLD 279

QY 353 DSDGSFFLYSKLTVDKSRWQGNVFCSSVMHEALHNHYTKSLSLSPG 400

```

Db 280 DVDGTFYSLAYDKARWDHGDKFECAMHEALHNNHYTKSISKTQG 327

Search completed: March 8, 2005, 14:46:13  
Job time : 18.3022 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 73.9563 Seconds  
(without alignments)  
2769.633 Million cell updates/sec

Title: US-09-389-782A-5

Perfect score: 2240

Sequence: 1 ETPPPKLYHDETSQHLIC.....VMHEALNHVYTKSLSLSPG 400

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1234	55.1	330	1 GC1_HUMAN	P01857 homo sapien
2	1234	55.1	465	2 Q6GMX6	Q6gmX6 homo sapien
3	1234	55.1	466	2 Q6IN78	Q6in78 homo sapien
4	1234	55.1	469	2 Q7Z7P5	Q7z7P5 homo sapien
5	1234	55.1	470	2 Q6PJA4	Q6pJa4 homo sapien
6	1234	55.1	470	2 Q7Z5W1	Q7z5W1 homo sapien
7	1234	55.1	472	2 Q6N089	Q6n089 homo sapien
8	1234	55.1	475	2 Q6GMW7	Q6gmW7 homo sapien
9	1234	55.1	476	2 Q6GMX1	Q6gmX1 homo sapien
10	1230	54.9	473	2 Q6P055	Q6p055 homo sapien
11	1230	54.9	475	2 Q6M206	Q6m206 homo sapien
12	1230	54.9	480	2 Q6N094	Q6n094 homo sapien
13	1230	54.9	481	2 Q6N097	Q6n097 homo sapien
14	1230	54.9	482	2 Q7Z351	Q7z351 homo sapien
15	1230	54.9	679	2 Q96PQ8	Q96pQ8 homo sapien
16	1228	54.8	348	2 Q6PXX1	Q6pXx1 homo sapien
17	1228	54.8	473	2 Q6M2V7	Q6m2V7 homo sapien
18	1228	54.8	478	2 Q6P181	Q6p181 homo sapien
19	1228	54.8	480	2 Q6P0F1	Q6p0F1 homo sapien
20	1228	54.8	544	2 Q6NPJ95	Q6npJ95 homo sapien
21	1227	54.8	466	2 Q6N096	Q6n096 homo sapien
22	1223	54.6	475	2 Q6N095	Q6n095 homo sapien
23	1212	54.1	487	2 Q652L2	Q652L2 mus sp. fv/
24	1154.5	51.5	354	2 Q86T72	Q86t72 homo sapien
25	1150.5	51.4	521	2 Q8N4Y9	Q8n4Y9 homo sapien
26	1149.5	51.3	518	2 Q6N030	Q6n030 homo sapien
27	1148.5	51.3	326	1 GC2_HUMAN	P01859 homo sapien
28	1148.5	51.3	417	2 Q6N093	Q6n093 homo sapien
29	1148	51.2	464	2 Q6MZU6	Q6mZu6 homo sapien
30	1144.5	51.1	509	2 Q8NF17	Q8nf17 homo sapien
31	1143.5	51.0	465	2 Q6P6C4	Q6p6C4 homo sapien

32	1136	50.7	327	1 GC4_HUMAN	P01861 homo sapien
33	1136	50.7	473	2 Q8T6C3	Q8t6C3 homo sapien
34	1134.5	50.6	493	2 Q68CN4	Q68cn4 homo sapien
35	1133.5	50.6	290	1 GC3_HUMAN	P01860 homo sapien
36	1127	50.3	476	2 Q6MZX7	Q6mzx7 homo sapien
37	1013	45.2	401	1 T11B_HUMAN	O00300 homo sapien
38	923	41.2	323	1 GC_RABIT	P01870 oryctolagus
39	918	41.0	337	2 Q95W34	Q95w34 equus cabal
40	904.5	40.4	329	1 GC2_CAVPO	P01862 cavia porce
41	897.5	40.1	401	2 Q6P112	Q6p112 mus musculu
42	893.5	39.9	401	1 T11B_MOUSE	O08712 mus musculu
43	877	39.2	401	1 T11B_RAT	O08727 rattus norv
44	850	37.9	470	2 Q7TMK1	Q7tmk1 mus musculu
45	847.5	37.8	329	1 GC3_MOUSE	P22436 mus musculu

#### ALIGNMENTS

#### RESULT 1

ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	1g gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079 (1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170 (1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181 (1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Penstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			

RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RN Biochemistry 9:3188-3196(1970).  
 RP [7]  
 RX DISULFIDE BONDS.  
 RA MEDLINE=77070267; PubMed=1002129;  
 RX Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RP [8]  
 RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RA MEDLINE=81208100; PubMed=7236608;  
 RX Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -1- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the  
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC G1M(3) marker and the G1M (non-1) markers.  
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
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 CC -----  
 DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
 DR PIR; A93433; GHHU.  
 DR PDB; 1AJ7; X-ray; H=1-103.  
 DR PDB; 1DSB; X-ray; B/H=1-101.  
 DR PDB; 1DS1; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1E4K; X-ray; A/B=106-329.  
 DR PDB; 1FC1; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCC; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I72; X-ray; B/D=1-103.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A/B=120-326.  
 DR PDB; 1QQX; X-ray; A/B=119-330.  
 DR PDB; 2RCS; X-ray; H=1-103.  
 DR Genew; HGNC:5525; IGHG1.  
 DR MIM; 147100; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; P:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG; 3.  
 DR PROSITE; PS50835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct protein sequencing; Glycoprotein;  
 Immunoglobulin C region; Immunoglobulin domain.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 Hinge.

FT	DOMAIN	111	223	CH2.
FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	
FT	DISULFID	103	103	
FT	DISULFID	109	109	Interchain (with light chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	Interchain (with heavy chain).
FT	DISULFID	250	308	
FT	CARBOHYD	180	180	
FT	VARIANT	97	97	N-linked (GlcNAc. . .).
FT	VARIANT	239	239	K -> R (in G1M(3) marker).
FT	VARIANT	241	241	/FTID=VAR_003886.
FT	VARIANT	241	241	D -> E (in G1M(non-1) marker).
FT	VARIANT	241	241	/FTID=VAR_003887.
FT	VARIANT	241	241	L -> M (in G1M(non-1) marker).
FT	VARIANT	241	241	/FTID=VAR_003888.
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	TURN	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELIX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	TURN	176	177	
FT	STRAND	179	180	
FT	STRAND	183	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELIX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 55.1%; Score 1234; DB 1; Length 330;  
 Best Local Similarity 92.1%; Pred. No. 3.2e-73;  
 Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

Qy	159	THDNICS-----GNSESTQKV-----DKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMIS	208
Db	78	TQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMIS	137

QY 209 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268  
 DB 138 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 197  
 QY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 328  
 DB 198 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 257  
 QY 329 SDIAVESNGQPNENYKTTTPPVLDSGSPFLYSLKTVDKSRWQGNVFSVCSVMHEALHN 388  
 DB 258 SDIAVESNGQPNENYKTTTPPVLDSGSPFLYSLKTVDKSRWQGNVFSVCSVMHEALHN 317  
 QY 389 HYTKQSLSLSPG 400  
 DB 318 HYTKQSLSLSPG 329

RESULT 2  
 Q6GMX6 PRELIMINARY; PRT; 465 AA.

AC Q6GMX6  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766; AAH73766.1; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; IG1.2.  
 DR SMART; SM00407; IG1; 3.  
 DR SMART; SM00406; IG1; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.

SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;  
 Query Match 55.1%; Score 1234; DB 2; Length 465;  
 Best Local Similarity 92.1%; Pred. No. 4.7e-73;  
 Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;  
 QY 159 THDNITCS-----GNSSESTOKV-----DKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 208  
 DB 213 TQYICNNVNHKPSNTKVDKKVPEKPSCKDTHHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 272  
 QY 209 RIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268  
 DB 273 RIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 332  
 QY 269 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 328  
 DB 333 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYP 392  
 QY 329 SDIAVESNGQPNENYKTTTPPVLDSGSPFLYSLKTVDKSRWQGNVFSVCSVMHEALHN 388  
 DB 393 SDIAVESNGQPNENYKTTTPPVLDSGSPFLYSLKTVDKSRWQGNVFSVCSVMHEALHN 452  
 QY 389 HYTKQSLSLSPG 400  
 DB 453 HYTKQSLSLSPG 464

RESULT 3  
 Q6IN78 PRELIMINARY; PRT; 466 AA.

AC Q6IN78  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE IGHG1 protein.  
 GN Name=IGHG1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

SEQUENCE FROM N.A.  
 RP TISSUE=Peripheral Nervous System;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

SEQUENCE FROM N.A.  
 RP TISSUE=Peripheral Nervous System;  
 RC Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC072419; AAH72419.1; -;  
 DR HSSP; P01861; 1ADO.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.



RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018747; AAH18747.1; -;  
DR HSP; P01861; IADO.  
DR InterPro; IPR003599; Ig\_LIKE.  
DR InterPro; IPR007110; Ig\_LIKE.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11PD7D99 CRC64;  
Query Match 55.1%; Score 1234; DB 2; Length 470;  
Best Local Similarity 92.1%; Pred. No. 4.8e-73;  
Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;  
QY 159 THDNICS-----GNSSESTQKV-----DKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 208  
DB 218 TQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 277  
QY 209 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWL 268  
DB 278 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWL 337  
QY 269 NGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328  
DB 338 NGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397  
QY 329 SDTAVESNGQPNKYKTPPPVLDSDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHN 388  
DB 398 SDTAVESNGQPNKYKTPPPVLDSDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHN 457  
QY 389 HYTKQSLSLSPG 400  
DB 458 HYTKQSLSLSPG 469  
RESULT 6  
ID Q725W1 PRELIMINARY; PRT; 470 AA.  
AC Q725W1;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAH53984.1; -;  
DR HSP; P01857; IHZH.  
DR InterPro; IPR007110; Ig\_LIKE.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483B1A CRC64;  
Query Match 55.1%; Score 1234; DB 2; Length 470;  
Best Local Similarity 92.1%; Pred. No. 4.8e-73;  
Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;  
QY 159 THDNICS-----GNSSESTQKV-----DKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 208  
DB 218 TQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGGPSVLPFPKPKDTLMIS 277  
QY 209 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWL 268  
DB 278 RTEPVTCTVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDWL 337  
QY 269 NGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328  
DB 338 NGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397  
QY 329 SDTAVESNGQPNKYKTPPPVLDSDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHN 388  
DB 398 SDTAVESNGQPNKYKTPPPVLDSDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHN 457  
QY 389 HYTKQSLSLSPG 400  
DB 458 HYTKQSLSLSPG 469  
RESULT 7  
ID Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686P15220.  
GN Name=DKFZp686P15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;

RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640627; CAE45781.1; -;  
 DR HSSP; P01861; 1ADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.cl.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG.MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 55.1%; Score 1234; DB 2; Length 472;  
 Best Local Similarity 92.5%; Pred. No. 4.8e-73;  
 Matches 233; Conservative 2; Mismatches 7; Indels 10; Gaps 2;

QY 159 THDNICSGSE-STQKV-----DKHTCCPCPAPPELLGGPSVFLPPKPKDTLMIS 208  
 DB 220 TQTYICNVNHPSTKVDKRVKPSCKDHTCCPCPAPPELLGGPSVFLPPKPKDTLMIS 279  
 QY 209 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWL 268  
 DB 280 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWL 339  
 QY 269 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 328  
 DB 340 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 399  
 QY 329 SDIAVESNGQPNENYKTTTPVLDSDGSPFLYSKLTVDKSRWQGNVFSVNMHEALHN 388  
 DB 400 SDIAVESNGQPNENYKTTTPVLDSDGSPFLYSKLTVDKSRWQGNVFSVNMHEALHN 459  
 QY 389 HYTKSLSLSPG 400  
 DB 460 HYTKSLSLSPG 471

RESULT 8  
 Q6GMW7 PRELIMINARY; PRT; 475 AA.  
 ID Q6GMW7  
 AC Q6GMW7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073782; AAH73782.1; -;  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.cl.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00407; IG; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGC1; 3.  
 DR SMART; SM00407; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG.MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 475 AA; 51987 MW; 2A1FES5D736860F8 CRC64;

Query Match 55.1%; Score 1234; DB 2; Length 475;  
 Best Local Similarity 92.1%; Pred. No. 4.8e-73;  
 Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

QY 159 THDNICSGSE-STQKV-----DKHTCCPCPAPPELLGGPSVFLPPKPKDTLMIS 208  
 DB 223 TQTYICNVNHPSTKVDKRVKPSCKDHTCCPCPAPPELLGGPSVFLPPKPKDTLMIS 282  
 QY 209 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWL 268  
 DB 283 RTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWL 342  
 QY 269 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 328  
 DB 343 NGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYF 402  
 QY 329 SDIAVESNGQPNENYKTTTPVLDSDGSPFLYSKLTVDKSRWQGNVFSVNMHEALHN 388  
 DB 403 SDIAVESNGQPNENYKTTTPVLDSDGSPFLYSKLTVDKSRWQGNVFSVNMHEALHN 462  
 QY 389 HYTKSLSLSPG 400  
 DB 463 HYTKSLSLSPG 474

RESULT 9  
 Q6GMX1 PRELIMINARY; PRT; 476 AA.  
 ID Q6GMX1  
 AC Q6GMX1  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073773; AAH73773.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00407; IG1; 3.  
DR SMART; SM00406; IG1; 1.  
DR SMART; SM00407; IG1; 3.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;  
Query Match 55.1%; Score 1234; DB 2; Length 476;  
Best Local Similarity 92.1%; Pred. No. 4.8e-73;  
Matches 232; Conservative 4; Mismatches 6; Indels 10; Gaps 2;  
QY 159 THDNICS-----GNSESTQKV-----DKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 208  
DB 224 TQYICNVNHNKPSNTKVDKKVEPKSCDKTHKTPCCPAPPELLGGPSVFLPPKPKDTLMIS 283  
QY 209 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268  
DB 284 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 343  
QY 269 NGKEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328  
DB 344 NGKEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 403  
QY 329 SDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQOQGNVFSCSVHMEALHN 388  
DB 404 SDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQOQGNVFSCSVHMEALHN 463  
QY 389 HTQKSLSLSPG 400  
DB 464 HTQKSLSLSPG 475  
RESULT 10  
Q6P055 ID Q6P055 PRELIMINARY; PRT; 473 AA.  
AC Q6P055;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zerbberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC065820; AAH65820.1; -;  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG1; 3.  
DR SMART; SM00406; IG1; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;  
Query Match 54.9%; Score 1230; DB 2; Length 473;  
Best Local Similarity 91.7%; Pred. No. 8.8e-73;  
Matches 231; Conservative 4; Mismatches 7; Indels 10; Gaps 2;  
QY 159 THDNICS-----GNSESTQKV-----DKTHTCCPCAPPELLGGPSVFLPPKPKDTLMIS 208  
DB 221 TQYICNVNHNKPSNTKVDKKVEPKSCDKTHKTPCCPAPPELLGGPSVFLPPKPKDTLMIS 280  
QY 209 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 268  
DB 281 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 340  
QY 269 NGKEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328  
DB 341 NGKEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 400  
QY 329 SDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQOQGNVFSCSVHMEALHN 388  
DB 401 SDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQOQGNVFSCSVHMEALHN 460  
QY 389 HTQKSLSLSPG 400  
DB 461 HTQKSLSLSPG 472  
RESULT 11  
Q6WZQ6



DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF07654; Cl-set; 3.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGC1; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
SQ	SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;
Query Match 54.9%; Score 1230; DB 2; Length 481;	
Best Local Similarity 91.7%; Pred.No. 8.9e-73;	
Matches 231; Conservative 4; Mismatches 7; Indels 10; Gaps 2;	
QY	159 THDNICS-----GNSESTQKV-----DKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMIS 208    :::
Db	229 TQTYICNVNHKPSNTKVDKKVEPKSKCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMIS 288    :::
QY	209 RTPVETCVVVDSHEDPEVKFNWYVDGVEVHNNAKTTPREEQYNSTRYRVSVLTVLHQDWL 268 
Db	289 RTPVETCVVVDSHEDPEVKFNWYVDGVEVHNNAKTTPREEQYNSTRYRVSVLTVLHQDWL 348 
QY	269 NGKEYCKVSNKALPAPIEKTIISKAKGPDPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328 
Db	349 NGKEYCKVSNKALPAPIEKTIISKAKGPDPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 408 
QY	329 SDIAVWEESNGOPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 388 
Db	409 SDIAVWEESNGOPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHN 468 
QY	389 HYTKLSLSLSPG 400 
Db	469 HYTKLSLSLSPG 480 
RESULT 14	
Q72351	PRELIMINARY; PRT; 482 AA.
ID	Q72351
AC	Q72351
DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypochemical protein DKFZp686N02209.
GN	Names=DKFZp686N02209;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON	NCBI_TaxID=9606;
RX	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Human rectum tumor;
RA	Bloeker H., Boecker M., Meves H.W., Weil B., Amid C., Osanger A.,
RA	Fobo G., Han M., Wiemann S.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BX538118; CAD98026.1; -.
DR	HSSP; P01857; 1HZH.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; Cl-set; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
SQ	SEQUENCE 482 AA; 52852 MW; ED475F1901D1A034 CRC64;
Query Match 54.9%; Score 1230; DB 2; Length 482;	
Best Local Similarity 91.7%; Pred.No. 9e-73; 7; Indels 10; Gaps 2;	
Matches 231; Conservative 4; Mismatches 7; Indels 10; Gaps 2;	
QY	159 THDNICS-----GNSESTQKV-----DKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMIS 208    :::
Db	229 TQTYICNVNHKPSNTKVDKKVEPKSKCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMIS 288    :::
QY	209 RTPVETCVVVDSHEDPEVKFNWYVDGVEVHNNAKTTPREEQYNSTRYRVSVLTVLHQDWL 268 
Db	289 RTPVETCVVVDSHEDPEVKFNWYVDGVEVHNNAKTTPREEQYNSTRYRVSVLTVLHQDWL 348 
QY	269 NGKEYCKVSNKALPAPIEKTIISKAKGPDPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 328 
Db	349 NGKEYCKVSNKALPAPIEKTIISKAKGPDPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 408 
QY	329 SDIAVWEESNGOPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 388 
Db	409 SDIAVWEESNGOPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHN 468 
QY	389 HYTKLSLSLSPG 400 
Db	469 HYTKLSLSLSPG 480 
RESULT 15	
Q96PQ8	PRELIMINARY; PRT; 679 AA.
ID	Q96PQ8
AC	Q96PQ8
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Factor VII active site mutant immunoconjugate.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON	NCBI_TaxID=9606;
RX	[1]
RP	SEQUENCE FROM N.A.
RC	MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA	Hu Z., Garen A.;
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor
RT	cells for immunotherapy in mouse models of prostatic cancer.";
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Hu Z., Garen A.;
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF272774; AAK98686.2; -.
DR	HSSP; P08709; 1KLI.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005509; F:calcium ion binding; IEA.
DR	GO; GO:0008233; F:peptidase activity; IEA.
DR	GO; GO:0004295; F:trypsin activity; IEA.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR00152; Abx hydroxyl_s.
DR	InterPro; IPR00742; EGF_2.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR001254; Peptidase_S1.
DR	InterPro; IPR009003; Pept_Ser_Cys.
DR	Pfam; PF07654; Cl-set; 2.
DR	Pfam; PF00008; EGF; 1.
DR	Pfam; PF00594; Gla; 1.
DR	Pfam; PF00089; Trypsin; 1.
DR	SMART; SM00179; EGF_CA; 1.
DR	SMART; SM00069; GLA; 1.
DR	SMART; SM00407; IGC1; 1.
DR	SMART; SM00020; Tryp_SPC; 1.
DR	PROSITE; PS00010; ASK_HYDROXYL; UNKNOWN_1.
DR	PRO

DK PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLA\_1; 1.  
DR PROSITE; PS00011; GLA\_1; 1.

DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS0134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 54.9%; Score 1230; DB 2; Length 679;  
Best Local Similarity 97.4%; Pred. No. 1.3e-72;  
Matches 227; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 168 SESTQKVDKTHTCPPCPAPBLLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 227  
| : |||||  
Db 446 SAEPKSCDKTHTCPPCPAPBLLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 505  
|||  
QY 228 KFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 287  
|||  
Db 506 KFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 565  
|||  
QY 288 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 347  
|||  
Db 566 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 625  
|||  
QY 348 TPVLDSDGSGFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYTQKSLSLSPG 400  
|||  
Db 626 TPVLDSDGSGFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYTQKSLSLSPG 678  
|||

Search completed: March 8, 2005, 14:44:38  
Job time : 75.9563 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 85.1551 Seconds  
(without alignments)  
1843.986 Million cell updates/sec

Title: US-09-389-782a-6  
Perfect score: 2274  
Sequence: 1 ETPPPKYLHDETSQLLC.....VMHEALHNHYTKSLSPG 406

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2274	100.0	406	4 AAB80902	Aab80902 Human OPG
2	2274	100.0	406	4 AAY72920	Aay72920 Human OPG
3	2256.5	99.2	413	4 AAB80900	Aab80900 Human OPG
4	2256.5	99.2	413	4 AAY72918	Aay72918 Human ost
5	2227	97.9	400	4 AAB80901	Aab80901 Human OPG
6	2227	97.9	400	4 AAY72919	Aay72919 Human OPG
7	2227	97.9	422	4 AAB66993	Aab66993 OPG-Fc. 4
8	2226	97.9	425	5 ABG71831	Abg71831 Human OPG
9	2224.5	97.8	407	4 AAB80899	Aab80899 Human OPG
10	2224.5	97.8	407	4 AAY72917	Aay72917 Human ost
11	2191	96.4	404	4 AAB80903	Aab80903 Human OPG
12	2191	96.4	404	4 AAY72921	Aay72921 Human OPG
13	1521.5	66.9	659	6 ABJ37103	Abj37103 Concatame
14	1521.5	66.9	659	8 ADQ79910	Adq79910 Human tum
15	1516	66.7	489	8 ADM32913	Adm32913 Amino aci
16	1513.5	66.6	490	6 ABJ37099	Abj37099 Concatame
17	1513.5	66.6	490	8 ADQ79902	Adq79902 Human tum
18	1513.5	66.6	720	6 ABJ37101	Abj37101 Concatame
19	1513.5	66.6	720	8 ADQ79906	Adq79906 Human tum
20	1501	66.0	518	4 AAB50080	Aab50080 TNFR:Fc f
21	1501	66.0	518	4 AAB70001	Aab70001 sTNFR:Fc f
22	1490	65.5	485	2 AAR24016	Aar24016 Fusion pr
23	1487.5	65.4	450	7 ADL06639	Adl06639 sTNFR:II-I
24	1487	65.4	518	2 AAR51003	Aar51003 Sequence
25	1470.5	64.7	444	5 ABG71833	Abg71833 RANK bind

26	1468.5	64.6	440	7 ADJ66000	Adj66000 Herpes vi
27	1468.5	64.6	440	8 ADP03589	Adp03589 Infection
28	1460	64.2	439	8 ADQ47876	Ado47876 Alpha-Her
29	1458.5	64.1	443	6 ABP58181	Abp58181 Human RAN
30	1458.5	64.1	443	6 AAE34361	Aae34361 Human RAN
31	1421	62.5	443	7 ADB17000	Adb17000 Murine RA
32	1419.5	62.4	442	7 ADB17001	Adb17001 Human RAN
33	1419.5	62.4	443	7 ADB17002	Adb17002 Human RAN
34	1389.5	61.1	608	6 ABJ37102	Abj37102 Concatame
35	1389.5	61.1	608	8 ADQ79908	Adq79908 Human tum
36	1381.5	60.8	444	6 ABJ37098	Abj37098 Concatame
37	1381.5	60.8	444	8 ADQ79900	Adq79900 Human tum
38	1381.5	60.8	628	6 ABJ37100	Abj37100 Concatame
39	1381.5	60.8	628	8 ADQ79904	Adq79904 Human tum
40	1349	59.3	376	2 AAW60037	Aaw60037 Antigenic
41	1348.5	59.3	396	8 ADF57557	Adf57557 Mouse ymk
42	1339.5	58.9	445	7 ADL06637	Adl06637 sTNFR:IG
43	1338.5	58.9	398	7 ABW02717	Abw02717 Mouse tms
44	1338.5	58.9	398	8 ADJ45758	Adj45758 Murine tm
45	1334	58.7	376	2 AAW50287	Aaw50287 Human Fas

ALIGNMENTS

RESULT 1  
AAB80902  
ID AAB80902 standard; protein; 406: AA.  
XX  
AC AAB80902;  
XX

DT 31-MAY-2001 (first entry)  
XX  
DE Human OPG(22-201)-FcdeltaC fusion protein.  
XX

KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;  
KW osteoclast formation inhibition; bone resorption inhibition;  
KW immunoglobulin.  
XX  
OS Homo sapiens.  
XX  
PN WO200117543-A2.  
XX

PD 15-MAR-2001.  
XX  
PF 18-AUG-2000; 2000WO-US022806.  
XX

PR 03-SEP-1999; 99US-00389545.  
XX  
PA (AMGE-) AMGEN INC.  
XX

PI Dunstan CR;  
XX  
XX WPI; 2001-265936/27.  
DR

PT Preventing or treating lytic bone diseases, particularly associated with  
cancer or metastasis, by administering an osteoprotegrin polypeptide.  
XX  
XX Disclosure; Fig 6; 87pp; English.

PS The present invention relates to a method for the prevention or treatment  
of lytic bone disease or multiple myeloma. Also the method can be used  
for preventing metastasis of cancer to bone or osteosclerotic bone  
metastasis. The method comprises administering an OPG (osteoprotegrin)  
polypeptide or OPG fusion protein. The present sequence is one such OPG  
fusion protein. OPG inhibits formation of osteoclasts (and thus bone  
resorption) by blocking differentiation from monocytes/macrophage  
precursors. The OPG polypeptide can be used in a method of preventing or  
treating lytic bone disease, for preventing metastasis of cancer to bone  
(e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal  
tract, multiple myeloma or lymphoma) and preventing the osteosclerotic

bone metastasis. The OPG fusion polypeptides are used in the prevention or treatment of loss of bone mass, which occurs in conditions including osteoporosis, such as primary osteoporosis, endocrine osteoporosis (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta, homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis due to immobilisation of extremities; Paget's disease of bone (osteitis deformans) in adults and juveniles; osteomyelitis, or an infectious lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung and kidney) and haematologic malignancies (multiple myeloma, lymphoma and leukaemia); idiopathic hypercalcaemia, and hypercalcaemia associated with hyperthyroidism and renal function disorders; osteopaenia following surgery, induced by steroid administration, and associated with disorders of the small and large intestine and with chronic hepatic and renal diseases; osteonecrosis, or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus and other conditions; bone loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis; prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins are also used in the replacement of structurally sound bone with disorganised bone as seen in Paget's disease of bone (osteitis deformans) in adults and juveniles; hyperparathyroidism, in congenital bone disorders such as fibrous dysplasia, and in osteosclerotic bone metastases. The OPG fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity. The OPG fusion protein comprises a fragment of the human OPB protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and CH3 regions; see AAB80897-8)

XX SQ Sequence 406 AA;

Query Match 100.0%; Score 2274; DB 4; Length 406;  
Best Local Similarity 100.0%; Pred. No. 6.4e-131;  
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60  
DB 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60

QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERTV 120  
DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERTV 120

QY 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVT 180  
DB 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVT 180

QY 181 DKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYD 240  
DB 181 DKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYD 240

QY 241 GVEVHNKTPREQVNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAK 300  
DB 241 GVEVHNKTPREQVNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAK 300

QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTPPVLDS 360  
DB 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTPPVLDS 360

QY 361 DGSFFLYSKLTVDKSRWQQGNVFCFVSVWHEALHNHYTQKSLSLSPG 406  
DB 361 DGSFFLYSKLTVDKSRWQQGNVFCFVSVWHEALHNHYTQKSLSLSPG 406

## RESULT 2

AA72920  
ID AAY72920 standard; protein; 406 AA.  
XX  
AC AAY72920;  
XX  
DT 13-JUN-2001 (first entry)  
XX  
DE Human OPB (22-201 aa)-Fc region (lacking 1-5 residues) fusion protein.

XX KW Human; fusion protein; osteoprotegerin; OPB; Fc protein; osteopathic; therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis; hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis; osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1; periodontal.  
XX OS Homo sapiens.  
XX FH Key  
FT Region Location/Qualifiers  
FT 1.179 /note= "Derived from human osteoprotegerin fragment (22-201 residues)"  
FT 180 /label= Linker  
FT 181.406 /note= Human IgG1 Fc region lacking 1-5 residues; (Corresponds to 6-231 residues of IgG1 Fc region)  
XX WO200118203-A1.  
XX 15-MAR-2001.  
XX 18-AUG-2000; 2000WO-US022797.  
XX 03-SEP-1999; 99US-00389782.  
XX (AMGE-) AMGEN INC.  
XX Dunstan CR, Wooden SK, Mann MB;  
XX WPI; 2001-244572/25.  
XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.  
XX Claim 7; Fig 6; 119pp; English.  
XX The present sequence is a fusion protein comprising a sequence derived from human osteoprotegerin (OPB; 22-201 residues) which is fused with human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues, by a linker. OPB negatively regulates the formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPB-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening  
XX SQ Sequence 406 AA;

Query Match 100.0%; Score 2274; DB 4; Length 406;  
Best Local Similarity 100.0%; Pred. No. 6.4e-131;  
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60  
DB 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECL 60

QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERTV 120  
DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTTPERTV 120

QY 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVT 180  
DB 121 CKRCPGFFSNSTSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVT 180

QY 181 DKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYD 240  
DB 181 DKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYD 240

QY 241 GVEVHNKTPREQVNSTYRVVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAK 300

Db 241 GVEVHNKTPREQYNTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIERTISKAK 300  
Qy 301 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLD 360  
Db 301 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLD 360  
Qy 361 DGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 406  
Db 361 DGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 406

RESULT 3  
AAB80900  
ID AAB80900 standard; protein; 413 AA.

XX AAB80900;  
XX 31-MAY-2001 (first entry)  
XX Human OPG(22-201)-Fc fusion protein.  
XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
XX multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;  
XX osteoclast formation inhibition; bone resorption inhibition;  
XX immunoglobulin.  
XX Homo sapiens.  
XX WO200117543-A2.  
XX 15-MAR-2001.  
XX 18-AUG-2000; 2000WO-US022806.  
XX 03-SEP-1999; 99US-00389545.  
XX (AMGE-) AMGEN INC.  
XX Dunstan CR;  
XX WPI; 2001-265936/27.  
XX Preventing or treating lytic bone diseases, particularly associated with  
XX cancer or metastasis, by administering an osteoprotegerin polypeptide.  
XX Disclosure; Fig 4; 87pp; English.

XX The present invention relates to a method for the prevention or treatment  
XX of lytic bone disease or multiple myeloma. Also the method can be used  
XX for preventing metastasis of cancer to bone or osteosclerotic bone  
XX metastasis. The method comprises administering an OPG (osteoprotegerin)  
XX polypeptide or OPG fusion protein. The present sequence is one such OPG  
XX fusion protein. OPG inhibits formation of osteoclasts (and thus bone  
XX resorption) by blocking differentiation from monocytes/macrophage  
XX precursors. The OPG polypeptide can be used in a method of preventing or  
XX treating lytic bone disease, for preventing metastasis of cancer to bone  
XX (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
XX rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal  
XX tract, multiple myeloma or lymphoma) and preventing the osteosclerotic  
XX bone metastasis. The OPG fusion polypeptides are used in the prevention  
XX or treatment of loss of bone mass, which occurs in conditions including  
XX osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
XX (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
XX congenital forms of osteoporosis (osteogenesis imperfecta,  
XX homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
XX due to immobilisation of extremities; Paget's disease of bone (osteitis  
XX deformans) in adults and juveniles; osteomyelitis, or an infectious  
XX lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
XX and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
XX leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
XX hyperthyroidism and renal function disorders; osteopaenia following  
XX surgery, induced by steroid administration, and associated with disorders

CC of the small and large intestine and with chronic hepatic and renal  
CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
CC are also used in the replacement of structurally sound bone with  
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
CC in adults and juveniles; hyperparathyroidism, in congenital bone  
CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
CC metastases. The OPG fusion proteins can exhibit increased circulating  
CC half-lives and slower clearance times, thereby providing a more sustained  
CC activity. The OPG fusion protein comprises a fragment of the human OPG  
CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and  
CC CH3 regions; see AAB80897-8)  
XX  
XX SQ Sequence 413 AA;

Query Match 99.2%; Score 2256.5; DB 4; Length 413;  
Best Local Similarity 98.1%; Pred. NO. 7.7e-130;  
Matches 405; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
Qy 1 ETFPKYLHYDETSHTQLLDCKPPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60  
Db 1 ETFPKYLHYDETSHTQLLDCKPPGTYLKQHCCTAKWTVCAPCPDHYTDSWHTSDECL 60  
Qy 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVGAGTPERTV 120  
Db 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVGAGTPERTV 120  
Qy 121 CKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180  
Db 121 CKRCPDGPFNSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180  
Qy 181 -----DKTHTCPCPAPELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 233  
Db 181 AAEPKSCDTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 240  
Qy 234 KFNWYVDGVEVHNKATKPREEQYNSTYRVSVLTVLHQLDNLNGKCYKCKVSNKALPAPIE 293  
Db 241 KFNWYVDGVEVHNKATKPREEQYNSTYRVSVLTVLHQLDNLNGKCYKCKVSNKALPAPIE 300  
Qy 294 KTIISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKT 353  
Db 301 KTIISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKT 360  
Qy 354 TTPVLDSDGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 406  
Db 361 TTPVLDSDGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 413

RESULT 4  
AA72918  
ID AA72918 standard; protein; 413 AA.

XX AA72918;  
XX 13-JUN-2001 (first entry)  
XX Human osteoprotegerin (22-201 residues)-IgG1 Fc region fusion protein.  
XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
XX therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
XX hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
XX osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
XX periodontal.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX Region 1..179  
XX /note= "Derived from human osteoprotegerin fragment (22-  
XX 201 residues)"





KW ischaemia; Parkinson's disease.

XX Unidentified.

XX WO200103719-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-US018667.

XX 09-JUL-1999; 99US-00350670.

XX 09-DEC-1999; 99US-00457647.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX WPI; 2001-103031/11.

XX N-PSDB; AAF57869.

XX Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha.

XX Disclosure; Fig 29; 316pp; English.

XX The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAF66974-AAF66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock.

XX Sequence 422 AA;

Query Match 97.9%; Score 2227; DB 4; Length 422;  
 Best Local Similarity 98.5%; Pred. No. 5e-128;  
 Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 1 ETFPKYLHYDEETSHQLLDCPKPGTYLKQCHTAKWTVCAPCPDHYTDSWHTSDECL 60  
 DB 22 ETFPKYLHYDEETSHQLLDCPKPGTYLKQCHTAKWTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVCKELQYKQCNRNTHRVCECKGRYLEIEFCLKHRSCTPCPGVQAGTPTERTNV 120  
 DB 82 YCSPVCKELQYKQCNRNTHRVCECKGRYLEIEFCLKHRSCTPCPGVQAGTPTERTNV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSESTQKCGIDVTV 180  
 DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSESTQK-----V 195

QY 181 DKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240  
 DB 196 DKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 255

QY 241 GVEVHNATKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALPAPTEKTIISKAK 300  
 DB 256 GVEVHNATKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALPAPTEKTIISKAK 315

QY 301 GQPRPQVTLPPSRDELTKNQSITCLVKGPYPSPDIAVWESNGQPENNYKTPPPVLDLS 360  
 DB 316 GQPRPQVTLPPSRDELTKNQSITCLVKGPYPSPDIAVWESNGQPENNYKTPPPVLDLS 375

QY 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 406  
 DB 376 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 421

RESULT 8

ABG71831

ID ABG71831 standard; protein; 425 AA.

XX AC ABG71831;

XX 14-APR-2003 (first entry)

XX Human OPG protein for expression in mammalian cells.

XX RANKL; human receptor activator of NFkappaB; osteoprotegerin; OPG;  
 KW RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;  
 KW osteoporosis; bone disease; human.

XX Homo sapiens.

XX Synthetic.

XX WO200264782-A2.

XX 22-AUG-2002.

XX 08-FEB-2002; 2002WO-DK000090.

XX 09-FEB-2001; 2001DK-00000214.

XX 09-FEB-2001; 2001US-0267843P.

XX 23-MAR-2001; 2001DK-00000498.

XX 23-MAR-2001; 2001US-0278320P.

XX (MAY-) MAXYGEN HOLDINGS LTD.

XX Haaning JM, Halkier T;

XX WPI; 2002-691592/74.

XX N-PSDB; ABS56347.

XX Novel human receptor activator of NFkappaB (hRANK) or human osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for treating osteoporosis.

XX Example 4; Fig 12; 129pp; English.

XX This invention relates to a novel polypeptide having an amino acid sequence that is different from and is at least about 70% identical to the amino acid sequence of human receptor activator of NFkappaB (hRANK) or human osteoprotegerin (hOPG), and which has a binding affinity to RANK ligand (RANKL) that is at least as high as the binding affinity of hRANK or hOPG to RANKL, as determined by functional competition assay. The protein of the invention may have osteopathic activity and may act as a RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity inhibitor. The nucleotide sequence shown in the invention may be used in gene therapy. The protein of the invention or fusion proteins comprising this protein are useful as a pharmaceutical, and in the preparation of a medicament for treating or preventing osteoporosis, or other bone diseases or diseases associated with binding of RANKL to the RANK receptor. A host cell containing a vector expressing the protein is useful for producing a polypeptide having binding affinity to RANKL, where the host cell is a eukaryotic host cell capable of in vivo glycosylation, and/or the polypeptide is subjected to conjugation to a non-polypeptide moiety in vitro. The protein of the invention has increased functional in vivo half-life and/or serum half-life compared to hRANK or hOPG and has an improved binding affinity to RANKL compared to the binding affinity of hRANK or hOPG to RANKL, as determined by a functional competition assay. The present sequence represents a human OPG protein modified for expression in a mammalian system, this sequence has the human OPG protein fused to a Leu-Glu dipeptide and amino acid

```

CC residues 247-475 of human IGG1
XX Sequence 425 AA;
SQ

Query Match          97.9%; Score 2226; DB 5; Length 425;
Best Local Similarity 98.3%; Pred. No. 5.8e-128;
Matches 399; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKDCKPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 22 ETTPPKYLHYDEETSHQLLCKDCKPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 120
DB 82 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 141
QY 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSTQKCGIDVTV 180
DB 142 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSTQK--LEKSS 199
QY 181 DKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
DB 200 DKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 259
QY 241 GVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
DB 260 GVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 319
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 360
DB 320 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 379
QY 361 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPG 406
DB 380 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPG 425

RESULT 9
AAB80899
ID AAB80899 standard; protein; 407 AA.
XX
AC AAB80899;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human OPG (22-194)-Fc fusion protein.
XX
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.
XX
OS Homo sapiens.
XX
PN WO200117543-A2.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022806.
XX
PR 03-SEP-1999; 99US-00389545.
XX
PA (AMGE-) AMGEN INC.
XX
PI Dunstan CR;
XX
XX WPI; 2001-265936/27.
XX
XX Preventing or treating lytic bone diseases, particularly associated with
PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
XX
PS Disclosure; Fig 3; 87pp; English.
XX

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The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic bone metastasis. The OPG fusion polypeptides are used in the prevention or treatment of loss of bone mass, which occurs in conditions including osteoporosis, such as primary osteoporosis, endocrine osteoporosis (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta, homocystinuria, Menkes' syndrome and Riley-Day syndrome) and due to immobilisation of extremities; Paget's disease of bone (osteitis deformans) in adults and juveniles; osteomyelitis, or an infectious lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung and kidney) and haematologic malignancies (multiple myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with hyperthyroidism and renal function disorders; osteopaenia following surgery, induced by steroid administration, and associated with disorders of the small and large intestine and with chronic hepatic and renal diseases; osteonecrosis, or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus and other conditions; bone loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis; prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins are also used in the replacement of structurally sound bone with disorganised bone as seen in Paget's disease of bone (osteitis deformans) in adults and juveniles; hyperparathyroidism, in congenital bone disorders such as fibrous dysplasia, and in osteosclerotic bone metastases. The OPG fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity. The OPG fusion protein comprises a fragment of the human OPG protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and CH3 regions; see AAB80897-8)

Query Match 97.8%; Score 2224.5; DB 4; Length 407;  
Best Local Similarity 98.0%; Pred. No. 6.8e-128;  
Matches 399; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKDCKPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60  
DB 1 ETTPPKYLHYDEETSHQLLCKDCKPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60  
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 120  
DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGPGVVQAGTPERNTV 120  
QY 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSTQKCGID-VT 179  
DB 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSTQKAAEPKS 180  
QY 180 VDKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239  
DB 181 CDKHTHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 240  
QY 240 DGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 299  
DB 241 DGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300  
QY 300 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 359  
DB 301 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 360  
QY 360 SDGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPG 406



osteoporosis, such as primary osteoporosis, endocrine osteoporosis (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta, homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis due to immobilisation of extremities; Paget's disease of bone (osteitis deformans) in adults and juveniles; osteomyelitis, or an infectious lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung and kidney) and haematologic malignancies (multiple myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with hyperthyroidism and renal function disorders; osteopaenia following surgery, induced by steroid administration, and associated with disorders of the small and large intestine and with chronic hepatic and renal diseases; osteonecrosis, or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus and other conditions; bone loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis; prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins are also used in the replacement of structurally sound bone with disorganised bone as seen in Paget's disease of bone (osteitis deformans) in adults and juveniles; hyperparathyroidism, in congenital bone disorders such as fibrous dysplasia, and in osteosclerotic bone metastases. The OPG fusion proteins can exhibit increased circulating half-lives and slower clearance times, thereby providing a more sustained activity. The OPG fusion protein comprises a fragment of the human OPG protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and CH3 regions; see AAB80897-8)

Sequence 404 AA;

Query Match 96.4%; Score 2191; DB 4; Length 404;  
 Best Local Similarity 97.5%; Pred. No. 7.6e-126;  
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;  
 QY 1 ETTPPKYLHYDEETSHQLLCKDPPGYLKHQCTAKWKTVCAPCDHYTDSWHTSDECL 60  
 DB 1 ETTPPKYLHYDEETSHQLLCKDPPGYLKHQCTAKWKTVCAPCDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHRSCTPPGGVVOAGTPERNTV 120  
 DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHRSCTPPGGVVOAGTPERNTV 120  
 QY 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKCGIDVTV 180  
 DB 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKSG--GGG 178  
 QY 181 DKHTCTPCPAPPELLGGPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 240  
 DB 179 GGGGTCPCPAPPELLGGPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 238  
 QY 241 GVEVHNKTPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAK 300  
 DB 239 GVEVHNKTPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAK 298  
 QY 301 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360  
 DB 299 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 358  
 QY 361 DGSFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHHYTKQSLSPG 406  
 DB 359 DGSFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHHYTKQSLSPG 404

RESULT 12

AAV72921

ID AAV72921 standard; protein; 404 AA.

XX AAV72921;

AC AAV72921;

XX 13-JUN-2001 (first entry)

DT Human OPG (22-194 residues)-FcG10 fusion protein.

DE Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;

KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 XX periodontal.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .173  
 FT /note= "Derived from human osteoprotegerin fragment (22-194 residues)"  
 FT 174. .182  
 FT /label= Ser-(Gly)8 linker  
 FT Region 183. .404  
 FT /note= Corresponds to 10-231 residues of human IgG1 Fc region  
 WO200118203-A1.  
 PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-US022797.  
 XX  
 PR 03-SEP-1999; 99US-00389782.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Dunstan CR, Wooden SK, Mann MB;  
 XX  
 DR WPI; 2001-244572/25.  
 XX  
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 PS Claim 7; Fig 7; 119pp; English.  
 XX  
 CC The present sequence is a fusion protein comprising a sequence derived from human osteoprotegerin (OPG; 22-194 residues) which is fused with human immunoglobulin G1 (IgG1) FcG10 region (lacks 1-9 residues and has a Ser-(Gly)8 linker). OPG negatively regulates the formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening

Sequence 404 AA;

Query Match 96.4%; Score 2191; DB 4; Length 404;  
 Best Local Similarity 97.5%; Pred. No. 7.6e-126;  
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKDPPGYLKHQCTAKWKTVCAPCDHYTDSWHTSDECL 60  
 DB 1 ETTPPKYLHYDEETSHQLLCKDPPGYLKHQCTAKWKTVCAPCDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHRSCTPPGGVVOAGTPERNTV 120  
 DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHRSCTPPGGVVOAGTPERNTV 120  
 QY 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKCGIDVTV 180  
 DB 121 CKRCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGSESTQKSG--GGG 178  
 QY 181 DKHTCTPCPAPPELLGGPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 240  
 DB 179 GGGGTCPCPAPPELLGGPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 238  
 QY 241 GVEVHNKTPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAK 300  
 DB 239 GVEVHNKTPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAK 298

QY 301 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDLS 360  
 DB 299 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDLS 358  
 QY 361 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTKLSLSPG 406  
 DB 359 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTKLSLSPG 404

RESULT 13  
 ABJ37103  
 ID ABJ37103 standard; protein; 659 AA.  
 XX AC ABJ37103;  
 XX AC  
 XX DT 08-MAY-2003 (first entry)  
 XX DE Concatameric immunoadhesion human protein sequence SEQ ID NO 12.  
 XX KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;  
 KW KW antiarthritic; immunomodulator; concatameric protein; soluble domain;  
 KW KW dimeric protein; inflammation; septicemia; cytotoxicity;  
 KW KW rheumatoid arthritis; cachexia; inflammation; human.  
 XX OS Homo sapiens.  
 XX XX  
 XX FN WO2003010202-A1.  
 XX XX  
 XX PD 06-FEB-2003.  
 XX XX  
 XX PF 26-JUL-2002; 2002WO-KR001427.  
 XX XX  
 XX PR 26-JUL-2001; 2001KR-00045028.  
 XX XX  
 XX PA (MEDE-) MEDEXGEN CO LTD.  
 XX XX  
 XX PI Chung Y, Han J, Lee H, Choi E, Kim J;  
 XX DR WPI; 2003-229639/22.  
 XX DR N-PSDB; ABT32046.  
 XX XX  
 XX PT New concatameric protein having two soluble domains, useful for  
 PT PT diagnosing and treating disorders associated with the dimeric protein or  
 PT PT its glycosylated form, such as inflammation, septicemia, rheumatoid  
 PT PT arthritis and cachexia.  
 XX XX  
 XX PS Claim 27; Page 148-152; 21pp; English.  
 XX XX  
 XX CC The invention relates to a novel concatameric protein comprising two  
 CC CC soluble domains, in which an N-terminus of a soluble domain of a  
 CC CC biologically active protein is linked to a C-terminus of an identical  
 CC CC soluble domain or a different soluble domain of a biologically active  
 CC CC protein. The methods and compositions of the present invention are useful  
 CC CC for the diagnosis and treatment of disorders associated with dimeric  
 CC CC protein or its glycosylated form, such as inflammation, septicemia,  
 CC CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-  
 CC CC related diseases. This sequence represents the human concatameric protein  
 CC CC of the invention  
 XX SQ Sequence 659 AA;

Query Match 66.9%; Score 1521.5; DB 6; Length 659;  
 Best Local Similarity 65.6%; Pred. No. 1.1e-84;  
 Matches 296; Conservative 16; Mismatches 80; Indels 59; Gaps 5;

QY 9 HYDEBTSHQLCDKPPGYLYLKHQCTAKWKTVCAPDPHYHSDSWHTSDECLYCSPVCKE 68  
 DB 214 YDQ--TAQMCCSKSPGQHAHVFTKTSYDTCDSCEHSTYQLWNWPECLSCGRSS 271  
 QY 69 LQYVQECNRTNHRVCECKEGYLI-----EFLKHRSCTPPGVVQAGTPERTNYCK 122  
 DB 272 DQVETQACTREQNRICRCPGWYCALSKQEGRLCAPLKRCPGFGVARGPTGTSDDVCK 331

QY 123 RCPDGFPSNETSKAPCRKHTNCSYFGLLLTQKGNATHDNIC----- 164  
 DB 332 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 387  
 QY 165 --SGNSESTQKCGIDVTV-----DKTHTCPPCPAPELL 195  
 DB 388 PVSTRSQHTQPTPEPSTAPSTFLLPMGPPSPAEGSTGDAEPKSCDKHTTCCPAPELL 447  
 QY 196 GGPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 255  
 DB 448 GGPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 507  
 QY 256 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 315  
 DB 508 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 567  
 QY 316 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 375  
 DB 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 627  
 QY 376 RWOQGNVFSVCSVMHEALHNHYTKLSLSPG 406  
 DB 628 RWOQGNVFSVCSVMHEALHNHYTKLSLSPG 658

RESULT 14  
 ADQ79910  
 ID ADQ79910 standard; protein; 659 AA.  
 XX AC ADQ79910;  
 XX AC  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Human tumour necrosis factor receptor 2, mgTNFR2-TNFR2/Ig construct.  
 XX KW Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;  
 KW KW immunoglobulin; concatameric fused dimer protein; immunoadhesin;  
 KW KW Fc fragment; hinge.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX XX  
 XX PN KR2004009997-A.  
 XX PD 31-JAN-2004.  
 XX XX  
 XX PF 26-JUL-2002; 2002KR-00045921.  
 XX XX  
 XX PR 26-JUL-2002; 2002KR-00045921.  
 XX PA (MEDE-) MEDEXGEN INC.  
 XX XX  
 XX PI Choi EY, Han JU, Jung YH, Kim JM, Lee HJ;  
 XX DR WPI; 2004-458871/43.  
 XX DR N-PSDB; ADQ79909.  
 XX XX  
 XX PT Concatameric immunoadhesin.  
 XX PS Claim 27; SEQ ID NO 12; 129pp; Korean.  
 XX CC The invention relates to a concatameric fused dimer protein and  
 CC CC glycosylation modification protein providing concatameric immunoadhesin  
 CC CC with improved efficacy and stability. The concatameric protein is  
 CC CC characteristically formed by binding C-terminal of one biologically  
 CC CC active protein with N-terminal of same or different biologically active  
 CC CC protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and  
 CC CC CTLA4. Two monomer proteins which are formed by fusing the extracellular  
 CC CC region of a protein participating in the same immune reaction to an  
 CC CC immunoglobulin Fc fragment, bound together at a hinge region by  
 CC CC disulphide bond to give the concatameric fused dimer protein, wherein the  
 CC CC immunoglobulin is IgG. The present sequence represents a monomeric or



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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 22.1968 Seconds  
(without alignments)  
1365.399 Million cell updates/sec

Title: US-09-389-782A-6  
Perfect score: 2274  
Sequence: 1 ETTPPKYLHYDETSHQLC.....VMHEALHNHYTKSLSPG 406

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1507.5	66.3	486	1	US-08-243-010-1
2	1501	66.0	518	1	US-08-385-229-4
3	1501	66.0	518	4	US-09-579-845-1
4	1501	66.0	518	4	US-09-579-845-3
5	1349	59.3	360	3	US-09-180-100-11
6	1349	59.3	376	3	US-09-180-100-22
7	1338.5	58.9	398	4	US-09-612-033B-14
8	1330	58.5	438	1	US-08-097-827-11
9	1330	58.5	438	1	US-08-494-574-11
10	1311.5	57.7	424	3	US-09-333-593A-8
11	1263.5	55.6	911	2	US-08-484-438-10
12	1260	55.4	704	4	US-09-590-656-2
13	1260	55.4	704	4	US-09-733-764-2
14	1257.5	55.3	664	3	US-08-957-063-16
15	1257.5	55.3	664	3	US-09-487-685-16
16	1257.5	55.3	664	4	US-08-802-805D-16
17	1257.5	55.3	664	4	US-09-388-316C-16
18	1254.5	55.2	664	3	US-09-957-063-18
19	1254.5	55.2	664	3	US-09-487-685-18
20	1254.5	55.2	664	3	US-08-802-805D-18
21	1254.5	55.2	664	4	US-09-388-316C-18
22	1250	55.0	592	4	US-09-313-942-8
23	1247	54.8	397	4	US-09-854-864-18
24	1246.5	54.8	680	3	US-08-227-496C-15
25	1241	54.6	347	1	US-07-940-861-43
26	1241	54.6	347	1	US-08-459-512-43
27	1241	54.6	347	2	US-08-459-657-43

Query Match 66.3%; Score 1507.5; DB 1; Length 486;  
Best Local Similarity 64.5%; Pred. No. 9.1e-117;

28	1241	54.6	347	2	US-08-460-132-43	Sequence 43, Appl
29	1241	54.6	347	3	US-08-466-465-8	Sequence 8, Appl
30	1241	54.6	347	4	US-09-730-465-8	Sequence 8, Appl
31	1241	54.6	347	5	PCT-US92-02050-43	Sequence 43, Appl
32	1240.5	54.6	449	3	US-08-897-236-23	Sequence 23, Appl
33	1240.5	54.6	449	4	US-09-500-253B-23	Sequence 23, Appl
34	1239.5	54.5	283	4	US-09-854-864-9	Sequence 9, Appl
35	1239.5	54.5	784	4	US-09-313-942-30	Sequence 30, Appl
36	1238.5	54.5	455	4	US-09-773-877B-24	Sequence 24, Appl
37	1236.5	54.4	387	1	US-08-470-299-4	Sequence 4, Appl
38	1236.5	54.4	547	4	US-09-746-359A-54	Sequence 54, Appl
39	1236.5	54.4	571	4	US-09-746-359A-53	Sequence 53, Appl
40	1235	54.3	396	2	US-08-784-512-3	Sequence 3, Appl
41	1235	54.3	396	3	US-09-176-228-3	Sequence 3, Appl
42	1234.5	54.3	331	3	US-09-178-869-2	Sequence 2, Appl
43	1234.5	54.3	331	4	US-09-761-413-2	Sequence 2, Appl
44	1234.5	54.3	388	3	US-09-131-247-16	Sequence 16, Appl
45	1234.5	54.3	388	4	US-09-784-623-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-243-010-1  
; Sequence 1, Application US/08243010  
; Patent No. 5639597  
; GENERAL INFORMATION:  
; APPLICANT: Lauffer, Leander  
; APPLICANT: Zettlmeisel, Gerd  
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The  
; TITLE OF INVENTION: Production and Use Thereof  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/243,010  
; FILING DATE: 13-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/798,564  
; FILING DATE: 26-NOV-1991  
; APPLICATION NUMBER: DE P 40 37 837.3  
; FILING DATE: 28-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Einaudi, Carol P.  
; REGISTRATION NUMBER: 32,220  
; REFERENCE/DOCKET NUMBER: 02481-1132-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 486 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-243-010-1



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QY 69 LQVVKQECNTHRVCEKGRYLEI-----BFCLKHRSCTPPGFGVVGAGTPTERTVCK 122
Db 132 DQVETQACTREONRICTCRPGWTCALSKQSGCRLCAPLRKCRPGFGVARGTSTDVVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLLTQKGNATHDNIC-----164
Db 192 PCAPGTFSNTSTSDICRPHQICNVVAI-----PQNASMDAVCTSTPTSRMARGAVHLPQ 247
QY 165 --SGNSESTQKCGIDVTV-----DKTHTCCPPCPAPELLG 196
Db 248 PVSTRSQHTQTPETPSTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCCPPCPAPELLG 307
QY 197 GPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 256
Db 308 GPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 367
QY 257 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEKTIISKAKGQPRPQVYVTLPPSRD 316
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEKTIISKAKGQPRPQVYVTLPPSRD 427
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 376
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
QY 377 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 406
Db 488 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 517
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## RESULT 4

US-09-579-845-3

; Sequence 3, Application US/09579845

; Patent No. 6537540

; GENERAL INFORMATION:

; APPLICANT: Burestein, Haim

; APPLICANT: Stepan, Anthony M.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED

; TITLE OF INVENTION: DISORDERS

; FILE REFERENCE: 226272004420

; CURRENT APPLICATION NUMBER: US/09/579, 845

; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/150,688

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-579-845-3

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Query Match 66.0%; Score 1501; DB 4; Length 518;
Best Local Similarity 64.7%; Pred. No. 3.4e-116;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;
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QY 9 HYDEETSHQLLCKCPGTYLKHQCTAKMTCVACPDHYHYTDSWHTSDCLYCSVPCKE 68
Db 74 YIQD--TAQWCCSKCSGQHAQVFCITSDTVCDSCEDSTYTQLMWNVPECLSGSRCS 131
QY 69 LQVVKQECNTHRVCEKGRYLEI-----BFCLKHRSCTPPGFGVVGAGTPTERTVCK 122
Db 132 DQVETQACTREONRICTCRPGWTCALSKQSGCRLCAPLRKCRPGFGVARGTSTDVVCK 191
QY 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLLTQKGNATHDNIC-----164
Db 192 PCAPGTFSNTSTSDICRPHQICNVVAI-----PQNASMDAVCTSTPTSRMARGAVHLPQ 247
QY 165 --SGNSESTQKCGIDVTV-----DKTHTCCPPCPAPELLG 196
Db 248 PVSTRSQHTQTPETPSTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCCPPCPAPELLG 307
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QY 197 GPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 256
Db 308 GPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 367
QY 257 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEKTIISKAKGQPRPQVYVTLPPSRD 316
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEKTIISKAKGQPRPQVYVTLPPSRD 427
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 376
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
QY 377 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 406
Db 488 WQOQNVFSCSVMEALHNNHYTKQSLSLSPG 517
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## RESULT 5

US-09-180-100-11

; Sequence 11, Application US/09180100

; Patent No. 6306395

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, No. 6306395io

; APPLICANT: NAKAMURA, Shigekazu

; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

; FILE REFERENCE: 1110-207P

; CURRENT APPLICATION NUMBER: US/09/180,100

; CURRENT FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: PCT/JP97/01502

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 11

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-180-100-11

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Query Match 59.3%; Score 1349; DB 3; Length 360;
Best Local Similarity 56.3%; Pred. No. 8.5e-104;
Matches 270; Conservative 15; Mismatches 60; Indels 62; Gaps 9;
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QY 8 LHYDEETSHQLLCKCPGTYLKHQCTAKM-KTVACAPCPD-HYHYTDSWHTSDCLYCSVP 65
Db 7 LHHDGQFCHK-----PCPPGERKARDCTVNGDEPDVCVQCEGKEYTDKAHFSSKRCR-L 61
QY 66 CKELQVVKQES--CNRTHNRVCEKGRYLEIBFCLKHRSCTPP-----GFGVVGAGTPTERT 119
Db 62 CDGEGGLEVEINCTRTQNTKCRCKPNFCNSTVC---EHCDCPTCKEHLIKECTILTSNT 118
QY 120 VCKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLLTQKGNATHDNICSGNSESTQKCGIDVT 179
Db 119 KCKE--EGSRSNPKS-----132
QY 180 VNKTHCTCPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239
Db 133 CDKTHCTCPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 192
QY 240 DGVEVHNAAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEKTIISK 299
Db 193 DGVEVHNAAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEKTIISK 252
QY 300 KGQPREPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 359
Db 253 KGQPREPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 312
QY 360 SDGSFFLYSLKLTVDKSRWQOQNVFSCSVMEALHNNHYTKQSLSLSPG 406
Db 313 SDGSFFLYSLKLTVDKSRWQOQNVFSCSVMEALHNNHYTKQSLSLSPG 359
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## RESULT 6

US-09-180-100-22

; Sequence 22, Application US/09180100  
; Patent No. 6306395  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, No. 6306395io  
; APPLICANT: NAGATA, Shigekazu  
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
; FILE REFERENCE: 1110-207P  
; CURRENT APPLICATION NUMBER: US/09/180,100  
; EARLIER FILING DATE: 1998-11-02  
; EARLIER APPLICATION NUMBER: PCT/JP97/01502  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-180-100-22

Query Match 59.3%; Score 1349; DB 3; Length 376;  
Best Local Similarity 66.3%; Pred. No. 9e-104;  
Matches 270; Conservative 15; Mismatches 60; Indels 62; Gaps 9;

QY 8 LHYDEETSHLLCDKCPGPGYLYKHQHTAKW-KTVCAPCPD-HYTTSDSWTSDECLYCSPV 65  
DB 23 LHHGQFCHK-----PCPPGERKARDCTVNGDEPCVCGEGKEYTDKAHFSKRCR-L 77  
QY 66 CKELQVYKQE--CNRTNHRVCECKEGRYLEIEFCLKHSRSCPP-----GFGVVQAGTPERNT 119  
DB 78 CDEGHGLEVEINCTRTQNTKCRCKPNFCNSTVC---EHCDCPTCKEHIIECTLSNT 134  
QY 120 VKRCPCDGFPSNITSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 179  
DB 135 KCKE--EGSRNPKS----- 148  
QY 180 VDKHTTCCPCPAPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYV 239  
DB 149 CDKHTTCCPCPAPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYV 208  
QY 240 DGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKA 299  
DB 209 DGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKA 268  
QY 300 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEVESNGQPNNTKTPPVLD 359  
DB 269 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEVESNGQPNNTKTPPVLD 328  
QY 360 SDGSFPLYSLKLTVDKSRWQGNVFCVSNVMEALHNHYTKSLSLSPG 406  
DB 329 SDGSFPLYSLKLTVDKSRWQGNVFCVSNVMEALHNHYTKSLSLSPG 375

RESULT 7  
US-09-612-033B-14  
; Sequence 14, Application US/09612033B  
; Patent No. 6627199  
; GENERAL INFORMATION:  
; APPLICANT: Sarris, Chris  
; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
; TITLE OF INVENTION: tms2, a No. 6627199el Member of the TNF-Receptor Superfamily  
; TITLE OF INVENTION: of Genes  
; FILE REFERENCE: 01017/35434A  
; CURRENT APPLICATION NUMBER: US/09/612,033B  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,063  
; PRIOR FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 398  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein  
; OTHER INFORMATION: Consisting of Mus musculus sequences and  
; OTHER INFORMATION: Immunoglobulin sequences  
US-09-612-033B-14

Query Match 58.9%; Score 1338.5; DB 4; Length 398;  
Best Local Similarity 66.4%; Pred. No. 7.2e-103;  
Matches 263; Conservative 24; Mismatches 58; Indels 51; Gaps 7;

QY 12 ETSQHLICDKCPGPGYLYKHQHC-TAKWKTVCACPDHYTSDSWTSDECLYCSPVCKELQ 70  
DB 52 EYWSKDVCCNCSAGTFVKAPCEIPIHTQCEKCHPGTFTKDNVLDACILCS-TCDDQ 110  
QY 71 VYKQCNRTNHRVCECKEGRYLEIEFCLKHSRSCPPGFGVQAGTPERNTVCKRCPDGFPS 130  
DB 111 EMVADCSATSDRKQCQRTGLY-----YDPKF-----DESCRPTCKCPQ---- 149  
QY 131 NETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTVDKHTTCCPCP 190  
DB 150 -----GIPVQECNSTANTVCSVSNN-----VD-THTCPCP 181  
QY 191 APPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYVVGVEVHNATK 250  
DB 192 APPELLGGPSVFLPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYVVGVEVHNATK 241  
QY 251 PREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAGQPREPQVY 310  
DB 242 PREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAGQPREPQVY 301  
QY 311 LPPSRDELTKNOVSLTCLVKGFPSPDI AVEVESNGQPNNTKTPPVLDSDGSFPLYSLK 370  
DB 302 LPPSRDELTKNOVSLTCLVKGFPSPDI AVEVESNGQPNNTKTPPVLDSDGSFPLYSLK 361  
QY 371 TVDKSRWQGNVFCVSNVMEALHNHYTKSLSLSPG 406  
DB 362 TVDKSRWQGNVFCVSNVMEALHNHYTKSLSLSPG 397

RESULT 8  
US-097-827-11  
; Sequence 11, Application US/08097827  
; GENERAL INFORMATION:  
; APPLICANT: Baum, Peter  
; Goodwin, Ray  
; Fanslow, William  
; Gayle, Richard  
; TITLE OF INVENTION: Novel Cytokine Which is a Ligand for  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/097,827  
; FILING DATE: 23-Jul-1993  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2806  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0730  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:



US-09-333-593A-8

Query Match 57.7%; Score 1311.5; DB 3; Length 424;  
Best Local Similarity 67.4%; Pred. No. 1.3e-100;  
Matches 262; Conservative 16; Mismatches 60; Indels 51; Gaps 8;

QY 23 CPPTGTYLKQCTAKWTVACPC-DHYTDSWHTSDCLYSPVCKELQVVKQECNRTHN 81  
DB 81 CPPTGTHISED-----GRDCISCKYQDYSTQWMDLLFCLRCTR-CDSEVELSPCTTTRN 134  
QY 82 RVCECKEGRYLE---LEFCLKHS-CPPGFGVVQAGTPERTVCKPCDGFSSNETSSKA 137  
DB 135 TVCQCEGTREDSPEMCKRKTGCGPRGMVKVGDCTPMSDIEC----- 178  
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNCISGNSESTQKCGIDVTVDKTHCTPPCPAPELLGG 197  
DB 179 -VHKGSRSI-----EGRGTEPK-----SADKTHCTPPCPAPELLGG 214  
QY 198 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQYN 257  
DB 215 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQYN 274  
QY 258 STYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAGQPREQVYTLPSRDE 317  
DB 275 STYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAGQPREQVYTLPSRDE 334  
QY 318 LTRKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 377  
DB 335 LTRKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 394  
QY 378 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 406  
DB 395 QQGNVFCSCVMHEALHNHYTQKSLSLSPG 423

## RESULT 11

US-08-484-438-10  
; Sequence 10, Application US/08484438  
; Patent No. 5811098  
; Patent No. 5811098 5780031  
; GENERAL INFORMATION:  
; APPLICANT: Plowman, Gregory D.  
; APPLICANT: Culouscou, Jean-Michel  
; APPLICANT: Shoyab, Mohammed  
; APPLICANT: Siegall, Clay B.  
; APPLICANT: Hellstr m, Ingegerd  
; APPLICANT: Hellstr m, Karl E.  
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,438  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/323,442  
; FILING DATE: 14-OCT-1994  
; APPLICATION NUMBER: US 08/150,704  
; FILING DATE: 10-NOV-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/981,165

## RESULT 12

US-09-590-656-2  
; Sequence 2, Application US/09590656  
; Patent No. 6413932  
; GENERAL INFORMATION:  
; APPLICANT: Cerretti, Douglas P.  
; APPLICANT: Borges, Luis G.  
; APPLICANT: Fanslow, III, William C.  
; TITLE OF INVENTION: TEK ANTAGONISTS  
; FILE REFERENCE: 2900-A  
; CURRENT APPLICATION NUMBER: US/09/590,656  
; CURRENT FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/137,889  
; PRIOR FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2

FILING DATE: 24-NOV-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,972  
REFERENCE/DOCKET NUMBER: 5624-230  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 911 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-484-438-10

Query Match 55.6%; Score 1263.5; DB 2; Length 911;  
Best Local Similarity 59.0%; Pred. No. 3.5e-96;  
Matches 268; Conservative 23; Mismatches 46; Indels 115; Gaps 17;

QY 31 QHCTAKWTVACPCDPHYTDS--WHTS-DECLYC-----SPVCKELQVVKQECNRTHN 82  
DB 494 ENCTAE-GWVC-----NHLCSGDCGCGPGDCLSCRRFSRGRICIE----- 534  
QY 83 VCECKEGRYLE---FCLKHS-CPPGFGVVQAGT-----PERNTVC-----K 122  
DB 535 SCNLYDGBEFENGSGICVE---CDPQCEKMEGDLTCHGPGPDNCTKCSHPKDGPNCVE 591  
QY 123 RCPDGF-----FSNETSKAPCRKHTNCSVFGLLTO--KGNATHDNI---CSGNS 168  
DB 592 KCPDLOGANSFIPKYADPDRECHPC--HPNC-----TQCCNGPTSHDCLYYIYPTWTHS 642  
QY 169 -----ESTQKCGIDVTVDKTHCTPPCPAP 192  
DB 643 TLPQDPVKVKALEGFPRLVGPDPFGCABPANTFLDPEPKSC-----DKHTCTPPCPAP 696  
QY 193 ELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNAKTKPR 252  
DB 697 ELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNAKTKPR 756  
QY 253 EEQYNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAGQPREQVYTL 312  
DB 757 EEQYNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAGQPREQVYTL 816  
QY 313 PSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 372  
DB 817 PSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 876  
QY 373 DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 406  
DB 877 DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 910

US-09-590-656-2  
; Sequence 2, Application US/09590656  
; Patent No. 6413932  
; GENERAL INFORMATION:  
; APPLICANT: Cerretti, Douglas P.  
; APPLICANT: Borges, Luis G.  
; APPLICANT: Fanslow, III, William C.  
; TITLE OF INVENTION: TEK ANTAGONISTS  
; FILE REFERENCE: 2900-A  
; CURRENT APPLICATION NUMBER: US/09/590,656  
; CURRENT FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/137,889  
; PRIOR FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2

[illegible]



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 61.3439 Seconds  
(without alignments)  
2177.757 Million cell updates/sec

Title: US-09-389-782A-6

Perfect score: 2274

Sequence: 1 ETTPPKYLHYDETSHTQLLC.....VMHEALHNYTKSLSPG 406

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB-seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:
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  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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  - 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2274	100.0	406	10	US-09-389-782-6
2	2256.5	99.2	413	10	US-09-389-782-4
3	2227	97.9	400	10	US-09-389-782-5
4	2226	97.9	425	16	US-10-467-243-20
5	2224.5	97.8	407	10	US-09-389-782-3
6	2191	96.4	404	10	US-09-389-782-7
7	1521.5	66.9	659	14	US-10-363-427-12
8	1516	66.7	467	17	US-10-901-735-4
9	1513.5	66.6	490	14	US-10-363-427-4
10	1513.5	66.6	720	14	US-10-363-427-8
11	1501	66.0	518	14	US-10-313-852-1
12	1501	66.0	518	14	US-10-313-852-3
13	1501	66.0	518	14	US-10-314-033-1
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					Sequence 6, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 20, Appli
					Sequence 3, Appli
					Sequence 7, Appli
					Sequence 12, Appli
					Sequence 4, Appli
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					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 1, Appli

14	1501	66.0	518	14	US-10-314-033-3	Sequence 3, Appli
15	1501	66.0	518	15	US-10-423-507-1	Sequence 1, Appli
16	1470.5	64.7	444	16	US-10-467-243-24	Sequence 24, Appli
17	1458.5	64.1	443	14	US-10-151-071-5	Sequence 5, Appli
18	1458.5	64.1	443	14	US-10-166-232A-5	Sequence 5, Appli
19	1389.5	61.1	608	14	US-10-363-427-10	Sequence 10, Appli
20	1381.5	60.8	444	14	US-10-363-427-2	Sequence 2, Appli
21	1381.5	60.8	628	14	US-10-363-427-6	Sequence 6, Appli
22	1349	59.3	360	9	US-09-949-713-11	Sequence 11, Appli
23	1349	59.3	376	9	US-09-949-713-22	Sequence 22, Appli
24	1349	59.3	376	14	US-10-084-139-10	Sequence 10, Appli
25	1348.5	59.3	396	14	US-10-193-616-14	Sequence 14, Appli
26	1338.5	58.9	398	15	US-10-622-407-14	Sequence 14, Appli
27	1287.5	56.6	380	9	US-09-948-018-39	Sequence 39, Appli
28	1277	56.2	404	9	US-09-948-018-16	Sequence 16, Appli
29	1275	56.1	446	9	US-09-792-200B-10	Sequence 10, Appli
30	1268	55.8	334	15	US-10-258-368-8	Sequence 8, Appli
31	1268	55.8	366	15	US-10-258-368-6	Sequence 6, Appli
32	1261	55.5	542	9	US-09-792-200B-16	Sequence 16, Appli
33	1260	55.4	704	9	US-09-733-764-2	Sequence 2, Appli
34	1260	55.4	704	14	US-10-357-653-2	Sequence 2, Appli
35	1258	55.3	360	15	US-10-390-566-20	Sequence 20, Appli
36	1258	55.3	360	15	US-10-390-566-27	Sequence 27, Appli
37	1258	55.3	367	15	US-10-390-566-19	Sequence 19, Appli
38	1258	55.3	367	15	US-10-390-566-26	Sequence 26, Appli
39	1258	55.3	404	15	US-10-258-368-15	Sequence 15, Appli
40	1257.5	55.3	664	9	US-09-388-316-16	Sequence 16, Appli
41	1257.5	55.3	664	14	US-10-357-822-16	Sequence 7, Appli
42	1257	55.3	360	15	US-10-390-566-7	Sequence 7, Appli
43	1257	55.3	360	15	US-10-390-566-14	Sequence 14, Appli
44	1257	55.3	367	15	US-10-390-566-6	Sequence 6, Appli
45	1257	55.3	367	15	US-10-390-566-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1  
US-09-389-782-6  
; Sequence 6, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-389-782-6

Query Match	100.0%;	Score 2274;	DB 10;	Length 406;
Best Local Similarity	100.0%;	Pred. No. 1.4e-139;		
Matches 406;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	ETTPPKYLHYDETSHTQLLCDCPPGTYLKQHTAKWTKVCA	CPDPHYTDSWHTSDECL	60
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Db	61	YCSPVCKELOYVQKQENRTHNRVCECKEGYLEIEFCLKX	HRSCPPGFGVVGAGTPERTV	120
Qy	121	CKRCPDGFSTNETSSKAPCRKHTNCVSFGLLLTKGNATH	DNICSGNSESTQKCGIDVT	180
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Db 181 DKHTCCPCAPPELLGSPSVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240  
QY 241 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 300  
Db 241 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 300  
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360  
Db 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360  
QY 361 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHALHNNHYTKQSLSPG 406  
Db 361 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHALHNNHYTKQSLSPG 406

RESULT 2  
US-09-389-782-4  
; Sequence 4, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-4

Query Match 99.2%; Score 2256.5; DB 10; Length 413;  
Best Local Similarity 98.1%; Pred. No. 1.9e-138;  
Matches 405; Conservative 0; Mismatches 1; Indels 7; Gaps 1;  
QY 1 ETPFPKYLHYDEETSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCDPDHYTDSWHTSDECL 60  
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QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180  
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QY 181 -----DKHTCCPCAPPELLGSPSVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEV 233  
Db 181 AAEPSKCDKHTCCPCAPPELLGSPSVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEV 240  
QY 234 KENWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE 293  
Db 241 KENWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE 300  
QY 294 KTIISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 353  
Db 301 KTIISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 360  
QY 354 TTPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHALHNNHYTKQSLSPG 406  
Db 361 TTPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHALHNNHYTKQSLSPG 413

RESULT 3  
US-09-389-782-5  
; Sequence 5, Application US/09389782

; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-5

Query Match 97.9%; Score 2227; DB 10; Length 400;  
Best Local Similarity 98.5%; Pred. No. 1.5e-136;  
Matches 400; Conservative 0; Mismatches 0; Indels 6; Gaps 1;  
QY 1 ETPFPKYLHYDEETSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCDPDHYTDSWHTSDECL 60  
Db 1 ETPFPKYLHYDEETSHQLLCKDCPPGTLYLKQHTAKWKTVCAPCDPDHYTDSWHTSDECL 60  
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Db 175 DKHTCCPCAPPELLGSPSVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 234  
QY 241 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 300  
Db 235 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAK 294  
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 360  
Db 295 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 354  
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Db 355 DGSFFLYSKLTVDKSRWQOGNVFSCSVMHALHNNHYTKQSLSPG 400

RESULT 4  
US-10-467-243-20  
; Sequence 20, Application US/10467243  
; Publication No. US20040132971A1  
; GENERAL INFORMATION:  
; APPLICANT: Maxygen Holdings Ltd.  
; APPLICANT: Haaning, Jesper Mortensen  
; APPLICANT: Halkier, Torben  
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES  
; FILE REFERENCE: 0226w0310  
; CURRENT APPLICATION NUMBER: US/10/467,243  
; CURRENT FILING DATE: 2003-08-06  
; PRIOR APPLICATION NUMBER: DK PA 2001 00214  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/267,843  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: DK PA 2001 00498  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 60/278,320  
; PRIOR FILING DATE: 2001-03-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20

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; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19
US-10-467-243-20

Query Match      97.9%; Score 2226; DB 16; Length 425;
Best Local Similarity 98.3%; Pred. No. 1.9e-136;
Matches 399; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 22  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERNTV 120
DB 82  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERNTV 141
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180
DB 142 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQK--LEKSS 199
QY 181 DKHTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
DB 200 DKHTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 259
QY 241 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
DB 260 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 319
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
DB 320 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 379
QY 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 406
DB 380 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 425

RESULT 5
US-09-389-782-3
; Sequence 3, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match      97.8%; Score 2224.5; DB 10; Length 407;
Best Local Similarity 98.0%; Pred. No. 2.3e-136;
Matches 399; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERNTV 120
DB 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERNTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSG--GGG 178
QY 181 DKHTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
DB 179 GGGGTCCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 238
QY 241 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
DB 239 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 298
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
DB 299 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 358
QY 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 406
DB 359 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 404

RESULT 6
US-09-389-782-7
; Sequence 7, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-7

Query Match      96.4%; Score 2191; DB 10; Length 404;
Best Local Similarity 97.5%; Pred. No. 3.4e-134;
Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 1  ETFPKYLHYDEBTSQLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERNTV 120
DB 61  YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERNTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 180
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSG--GGG 178
QY 181 DKHTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240
DB 179 GGGGTCCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 238
QY 241 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300
DB 239 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 298
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
DB 299 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 358
QY 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 406
DB 359 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPG 404
```

RESULT 7  
 US-10-363-427-12  
 ; Sequence 12, Application US/10363427  
 ; Publication No. US20030195338A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MedExGen Inc.  
 ; APPLICANT: CHUNG, Yong Hoon  
 ; APPLICANT: HAN, Ji Woong  
 ; APPLICANT: LEE, Hye Ja  
 ; APPLICANT: CHOI, Eun Yong  
 ; APPLICANT: KIM, Jin Mi  
 ; APPLICANT: YIM, Soo Bin  
 ; TITLE OF INVENTION: Concatametric Immunoadhesion  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/363,427  
 ; CURRENT FILING DATE: 2003-02-28  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: KopatentIn 1.71  
 ; SEQ ID NO 12  
 ; LENGTH: 659  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-363-427-12  
  
 Query Match 66.9%; Score 1521.5; DB 14; Length 659;  
 Best Local Similarity 65.6%; Pred. No. 1.5e-90;  
 Matches 296; Conservative 16; Mismatches 80; Indels 59; Gaps 5;  
  
 QY 9 HYDEETSHQLLCKDPCPGTYLKQHTAKWKVACAPCPDHYVYDTSWHTSDCLYCSPVCKE 68  
 Db 214 YDQ--TAQMCCSKCSPGQAHKVFCTKTSDTVCDSCEDSTYTQLNNWVPECLSGRCSS 271  
  
 QY 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFLKHSRCPGPGVVOAGTPERNTVCK 122  
 Db 272 DQVETQACTREQNRICTCRPGHYCALSKQEGCRLCAPLRCRPGFGVARGTETSDVCK 331  
  
 QY 123 RCPDGFSSNETSSKAPCRKHTNCVFGLLLTQKGNATHDNTC----- 164  
 Db 332 PCAPGTFSNTSSDTCRPHQICNVVAI----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 387  
  
 QY 165 --SGNSESTQKCGIDVTV-----DKHTCCPCPAPELL 195  
 Db 388 PVSTRSQHTQPTPESTAPSTSLFLPMGPPAEGSTGDAEPKCDKTHTCPCPAPELL 447  
  
 QY 196 GGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 255  
 Db 448 GGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 507  
  
 QY 256 YNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 315  
 Db 508 YNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 567  
  
 QY 316 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKKS 375  
 Db 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKKS 627  
  
 QY 376 RMOQGNVFCSCVMHEALHNHYTQKSLSLSPG 406  
 Db 628 RMOQGNVFCSCVMHEALHNHYTQKSLSLSPG 658  
  
 RESULT 8  
 US-10-901-735-4  
 ; Sequence 4, Application US/10901735  
 ; Publication No. US20050032183A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMGEN, Inc.  
 ; APPLICANT: OSSUND, Timothy D.  
 ; APPLICANT: CLOGSTON, Christi  
 ; APPLICANT: CRAMPTON, Shon  
 ; APPLICANT: BASS, Randal  
 ; TITLE OF INVENTION: CRYSTALLINE POLYPEPTIDES  
 ; FILE REFERENCE: A-859



QY 257 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316  
Db 368 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPMQTKISKAKGQPREPQVYTLPPSRD 427  
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 376  
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487  
QY 377 WOQGNVFCSCVMHEALHNYTKQSLSPG 406  
Db 488 WOQGNVFCSCVMHEALHNYTKQSLSPG 517

RESULT 12  
US-10-313-852-3  
; Sequence 3, Application US/10313852  
; Publication No. US20030103942A1  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; APPLICANT: Stepan, Anthony M.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING  
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED  
; FILE REFERENCE: 226272004420  
; CURRENT APPLICATION NUMBER: US/10/313,852  
; PRIOR FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: 60/150,845  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/150,688  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-313-852-3

Query Match 66.0%; Score 1501; DB 14; Length 518;  
Best Local Similarity 64.7%; Pred. No. 2.4e-89;  
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDETSQLLCDKCPGTYLKHCTAKWKTCVACPCPDHYVYDTSWHTSDECLYCSPVCKE 68  
Db 74 YDQ--TAQMCCKSCSPGQAHKVFCTKTSVDCSDSTYTLQMNWVPECLSCGSRCS 131  
QY 69 LQYVQECNTHNRVCECKEGRYLEI-----EFLKHSRCPFGVGVQAGTPERNTVCK 122  
Db 132 DQVETOACTREONRICTCRPGWCALSKQEGCRLCAPLRCRPGFVGVARPGTETSDVCK 191  
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHNIC----- 164  
Db 192 PCAGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247  
QY 165 --SGNSESTQKCGIDVTV-----DKHTCCPCPAPPELLG 196  
Db 248 PVSTRSQHTQTPERPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCCPAPPELLG 307  
QY 197 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 256  
Db 308 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 367  
QY 257 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316  
Db 368 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPMQTKISKAKGQPREPQVYTLPPSRD 427  
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 376  
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487  
QY 377 WOQGNVFCSCVMHEALHNYTKQSLSPG 406  
Db 488 WOQGNVFCSCVMHEALHNYTKQSLSPG 517

RESULT 14  
US-10-314-033-3  
; Sequence 3, Application US/10314033  
; Publication No. US20030113295A1  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; APPLICANT: Stepan, Anthony M.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING

Db 488 WOQGNVFCSCVMHEALHNYTKQSLSPG 517

RESULT 13  
US-10-314-033-1  
; Sequence 1, Application US/10314033  
; Publication No. US20030113295A1  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Haim  
; APPLICANT: Stepan, Anthony M.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING  
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED  
; FILE REFERENCE: 226272004420  
; CURRENT APPLICATION NUMBER: US/10/314,033  
; PRIOR FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US/09/579,845  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/150,688  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-314-033-1

Query Match 66.0%; Score 1501; DB 14; Length 518;  
Best Local Similarity 64.7%; Pred. No. 2.4e-89;  
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDETSQLLCDKCPGTYLKHCTAKWKTCVACPCPDHYVYDTSWHTSDECLYCSPVCKE 68  
Db 74 YDQ--TAQMCCKSCSPGQAHKVFCTKTSVDCSDSTYTLQMNWVPECLSCGSRCS 131  
QY 69 LQYVQECNTHNRVCECKEGRYLEI-----EFLKHSRCPFGVGVQAGTPERNTVCK 122  
Db 132 DQVETOACTREONRICTCRPGWCALSKQEGCRLCAPLRCRPGFVGVARPGTETSDVCK 191  
QY 123 RCPDGFNETSSKAPCRKHTNCSVFGLLLTQKGNATHNIC----- 164  
Db 192 PCAGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247  
QY 165 --SGNSESTQKCGIDVTV-----DKHTCCPCPAPPELLG 196  
Db 248 PVSTRSQHTQTPERPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCCPAPPELLG 307  
QY 197 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 256  
Db 308 GPSVFLPPPKDQTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 367  
QY 257 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 316  
Db 368 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPMQTKISKAKGQPREPQVYTLPPSRD 427  
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 376  
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487  
QY 377 WOQGNVFCSCVMHEALHNYTKQSLSPG 406  
Db 488 WOQGNVFCSCVMHEALHNYTKQSLSPG 517

```
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/314,033
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-314-033-3

Query Match      66.0%; Score 1501; DB 14; Length 518;
Best Local Similarity 64.7%; Pred. No. 2.4e-89;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDEETSHQLCDKCPGGTYLKHQHTAKWKTCVACPCPDHYHSDSWHTSDECLYCSPVCKE 68
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 74 YYDQ--TAQMCCKSGSPGQHAQVCTKTSDTVCDSCDSTYTQLMNVVPECLSCGRCSS 131
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 69 LQYVQECNRTNHRVCECKEGRYLEI-----EFLKHSRCPGPGVGVQAGTPERTNVCK 122
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 132 DQVETOACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFVGARPGTETSDVVC 191
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 123 RCPDGFPSNETSKAPCRKHTNCVFGLLLTQKGNATHDNIC----- 164
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 165 --SGNSESTQKCGIDVTV-----DKHTCTCPCPAPELLG 196
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 248 PVSTRSQHTQPTPEPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCCPPAPELLG 307
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 197 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 256
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 308 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 367
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 257 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRD 316
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMQKTISKAKGQPRPQVYTLPPSRD 427
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 376
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 428 ELTKNQVSLTCLVKGFYPRHIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 377 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 406
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:

RESULT 15
US-10-423-507-1
; Sequence 1, Application US/10423507
; Publication No. US20030219735A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Barrie, J.
; TITLE OF INVENTION: METABOLICALLY ACTIVATED RECOMBINANT
; FILE REFERENCE: 226272004302
; CURRENT APPLICATION NUMBER: US/10/423,507
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 09/634,126
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 60/160,080
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-423-507-1

Query Match      66.0%; Score 1501; DB 15; Length 518;
Best Local Similarity 64.7%; Pred. No. 2.4e-89;
Matches 291; Conservative 19; Mismatches 82; Indels 58; Gaps 5;

QY 9 HYDEETSHQLCDKCPGGTYLKHQHTAKWKTCVACPCPDHYHSDSWHTSDECLYCSPVCKE 68
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 74 YYDQ--TAQMCCKSGSPGQHAQVCTKTSDTVCDSCDSTYTQLMNVVPECLSCGRCSS 131
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 69 LQYVQECNRTNHRVCECKEGRYLEI-----EFLKHSRCPGPGVGVQAGTPERTNVCK 122
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 132 DQVETOACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFVGARPGTETSDVVC 191
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 123 RCPDGFPSNETSKAPCRKHTNCVFGLLLTQKGNATHDNIC----- 164
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 165 --SGNSESTQKCGIDVTV-----DKHTCTCPCPAPELLG 196
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 248 PVSTRSQHTQPTPEPSTAPSTSFLLPMGSPPAEGSTGDEPKSCDKTHTCCPPAPELLG 307
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 197 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 256
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 308 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 367
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 257 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRD 316
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 368 NSTYRVSVLTVLHODWLNKGYCKVSNKALPAPMQKTISKAKGQPRPQVYTLPPSRD 427
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 317 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 376
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 428 ELTKNQVSLTCLVKGFYPRHIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 377 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 406
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517
   :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:

Search completed: March 8, 2005, 15:16:08
Job time : 66.3439 secs
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## Igen Primaerstruktur.

A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668  
A;Molecule type: protein  
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
A;Note: this sequence has the G1m(17) and G1m(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KOI; disulfide bonds  
A;Accession: A91723  
A;Molecule type: protein  
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH  
A;Note: this sequence has the G1m(3) and G1m(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1002129  
A;Contents: annotation; disulfide bonds  
A;Genetics:  
A;Gene: IGHG1  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 114/1; 224/1  
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;137-206/Domain: immunoglobulin homology <IM2>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83,144-204,250-308/Disulfide bonds: #status experimental  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.1%; Score 1231; DB 1; Length 330;  
Best Local Similarity 92.5%; Pred. No. 9.6e-68;  
Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;

QY 159 THDNICGNSE-STOKCGIDV---TVDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMTS 214

Db 78 TQYICNVNHPKSNTKVDKKVFPKSCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMTS 137

QY 215 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWL 274

Db 138 RPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWL 197

QY 275 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGY 334

Db 198 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGY 257

QY 335 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVVHEALHN 394

Db 258 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVVHEALHN 317

QY 395 HVTQKSLSLSPG 406

Db 318 HVTQKSLSLSPG 329

RESULT 2

Ig gamma-1 chain C region - synthetic

C;Species: synthetic

A;Note: Homo sapiens (man) Gene engineered and expressed in Escherichia coli  
C;Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
A;Accession: S31866  
R;Filpula, D.

submitted to the EMBL Data Library, February 1993

A;Description: Screening method for protein-protein interactions of cloned gene products

A;Reference number: S31866

A;Accession: S31866

A;Molecule type: mRNA

A;Residues: 1-255 <PIL>

A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C;Keywords: immunoglobulin

F;1-22/Region: Escherichia coli outer membrane protein A precursor

F;23-255/Region: human Ig gamma-1 chain C region

Query Match 54.0%; Score 1228; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 1.1e-67;  
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 DKHTCTCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 240

Db 29 DKHTCTCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 88

QY 241 GVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 300

Db 89 GVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 148

QY 301 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPVLD 360

Db 149 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPVLD 208

QY 361 DGSFFLYSKLTVDKSRWQQGNVFCSVVHEALHNHYTQKSLSLSPG 406

Db 209 DGSFFLYSKLTVDKSRWQQGNVFCSVVHEALHNHYTQKSLSLSPG 254

RESULT 3

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000

A;Accession: S69339; S72664

R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A;Reference number: S69339; MUID:95262687; PMID:7744049

A;Accession: S69339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <KHA>

A;Cross-references: EMBL:X81695

R;Khamilichi, A.A.

submitted to the EMBL Data Library, September 1994

A;Reference number: S72664

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140,'C',142-374 <KH2>

A;Cross-references: EMBL:X81695

C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 53.8%; Score 1222.5; DB 2; Length 374;  
Best Local Similarity 95.4%; Pred. No. 3.6e-67;  
Matches 228; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

QY 175 GIDVTV-----DKHTCTCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVD 227

Db 135 GTLVTVSSSEPKSCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVD 194

QY 228 HEDPEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKA 287

Db 195 HEDPEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKA 254

QY 288 LPAPIEKTISKAKGPQREPOVYTLPPSRDELTKNOVSLCLVKGFYPSDIAVWESNGQP 347  
 Db 255 LPAPIEKTISKAKGPQREPOVYTLPPSRDEMTKNQVSLCLVKGFYPSDIAVWESNGQP 314  
 QY 348 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 406  
 Db 315 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 373

## RESULT 4

PT0207  
 Ig gamma chain C region - chimpanzee  
 C:Species: Pan troglodytes (Chimpanzee)  
 C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
 C:Accession: PT0207  
 R:Rhrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
 Mol. Immunol. 28, 319-322, 1991  
 A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
 A:Reference number: PT0207; MUID:91287716; PMID:2062315  
 A:Accession: PT0207  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <EHR>  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 1180; DB 2; Length 234;  
 Best Local Similarity 98.6%; Pred. No. 8.3e-65;  
 Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 181 DKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240  
 Db 15 DTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74  
 QY 241 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300  
 Db 75 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134  
 QY 301 GQPREPOVYTLPPSRDELTKNOVSLCLVKGFYPSDIAVWESNGQENNYKTTTPVLD 360  
 Db 135 GQPREPOVYTLPPSRDELTKNOVSLCLVKGFYPSDIAVWESNGQENNYKTTTPVLD 194  
 QY 361 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKS 400  
 Db 195 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKS 234

## RESULT 5

A23511  
 Ig gamma-3 chain C region (allotype G3m(b)) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
 C:Accession: A23511  
 R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
 Nucleic Acids Res. 14, 1779-1789, 1986  
 A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: ccd  
 A:Reference number: A23511; MUID:86148507; PMID:3081877  
 A:Accession: A23511  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056  
 C:Genetics:  
 A:Gene: GDB:IGHG3  
 A:Cross-references: GDB:119339; OMIM:147120  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.8%; Score 1156; DB 2; Length 377;  
 Best Local Similarity 74.3%; Pred. No. 3.9e-63;  
 Matches 223; Conservative 16; Mismatches 37; Indels 24; Gaps 4;

QY 110 VOAGTPERNT--VCKRCPDGPFNSNETSKAP--CRKHTNCSVFGLLLTQKGNATHDNICSG 166  
 Db 98 VELKTPGLDTHTCPCPEP-KSCDTPPCPCPEPKSCD----- 136  
 QY 167 NSESTQKCGIDVTVDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDV 226  
 Db 137 TTPPCPCPEPKSCDTPPCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDV 196  
 QY 227 SHEDPEVKFNWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 286  
 Db 197 SHEDPEVKFNWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 256  
 QY 287 ALPAPIEKTISKAKGPQREPOVYTLPPSRDELTKNOVSLCLVKGFYPSDIAVWESNGQ 346  
 Db 257 ALPAPIEKTISKAKGPQREPOVYTLPPSRDEMTKNQVSLCLVKGFYPSDIAVWESNGQ 316  
 QY 347 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 406  
 Db 317 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 376

## RESULT 6

A60764  
 Ig gamma-3 chain C region, form LAT - human  
 C:Species: Homo sapiens (man)  
 C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
 C:Accession: A60764  
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
 Immunogenetics 30, 250-257, 1989  
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGH4 convert  
 A:Reference number: A60764; MUID:90007613; PMID:2571587  
 A:Accession: A60764  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 A:Cross-references: UNIPROT:Q8N4Y9  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.7%; Score 1154; DB 2; Length 377;  
 Best Local Similarity 74.3%; Pred. No. 5.1e-63;  
 Matches 223; Conservative 16; Mismatches 37; Indels 24; Gaps 4;

QY 110 VOAGTPERNT--VCKRCPDGPFNSNETSKAP--CRKHTNCSVFGLLLTQKGNATHDNICSG 166  
 Db 98 VELKTPGLDTHTCPCPEP-KSCDTPPCPCPEPKSCD----- 136  
 QY 167 NSESTQKCGIDVTVDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDV 226  
 Db 137 TTPPCPCPEPKSCDTPPCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDV 196  
 QY 227 SHEDPEVKFNWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 286  
 Db 197 SHEDPEVKFNWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 256  
 QY 287 ALPAPIEKTISKAKGPQREPOVYTLPPSRDELTKNOVSLCLVKGFYPSDIAVWESNGQ 346  
 Db 257 ALPAPIEKTISKAKGPQREPOVYTLPPSRDEMTKNQVSLCLVKGFYPSDIAVWESNGQ 316  
 QY 347 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 406  
 Db 317 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 376

## RESULT 7

G2HU  
 Ig gamma-2 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
 C:Accession: A93906; A92809; A90752; A93132; A02148  
 R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
 A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
 A:Reference number: A93906; MUID:82197621; PMID:6804948  
 A:Accession: A93906  
 A:Molecule type: DNA  
 A:Residues: 1-326 <ELL>  
 A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; F  
 A:Note: Lys-326 is probably removed posttranslationally  
 R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
 J. Immunol. 125, 1048-1054, 1980  
 A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
 A:Reference number: A92809; MUID:81007873; PMID:6774012  
 A:Contents: myeloma protein TII  
 A:Accession: A92809  
 A:Molecule type: protein  
 A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
 A:Note: Trp-156 is at or near the complement-binding site  
 R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
 Can. J. Biochem. 57, 758-767, 1979  
 A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
 A:Reference number: A90752; MUID:80001357; PMID:113060  
 A:Contents: myeloma protein Zie  
 A:Accession: A90752  
 A:Molecule type: protein  
 A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
 A:Note: this sequence has since been revised  
 R:Hofmann, T.; Parr, D.M.  
 Mol. Immunol. 16, 923-925, 1979  
 A:Title: A note on the amino acid sequence of residues 391-391 of human immunoglobulin G  
 A:Reference number: A93132; MUID:80114419; PMID:118920  
 A:Contents: Zie  
 A:Accession: A93132  
 A:Molecule type: protein  
 A:Residues: 238-275 <HOF>  
 R:Hofmann, T.; Parr, D.M.  
 submitted to the Atlas, March 1980  
 A:Reference number: A94591  
 A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
 A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati  
 ned  
 R:Milstein, C.; Frangione, B.  
 Biochem. J. 121, 217-225, 1971  
 A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
 A:Reference number: A90253; MUID:72033500; PMID:4940472  
 A:Contents: annotation; myeloma protein Sa, disulfide bonds  
 R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
 Nature 221, 145-148, 1969  
 A:Title: Structural studies of immunoglobulin G.  
 A:Reference number: A93157; MUID:69064124; PMID:5782707  
 A:Contents: annotation; Sa, disulfide bonds  
 C:Genetics:  
 A:Gene: GDB:IGHG2  
 A:Cross-references: GDB:119338; OMIM:147110  
 A:Map position: 14q32.33-14q32.33  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:133-202/Domain: immunoglobulin homology <IM2>  
 F:239-306/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 50.5%; Score 1148; DB 1; Length 326;  
 Best Local Similarity 87.0%; Pred. No. 1e-62;  
 Matches 215; Conservative 9; Mismatches 11; Indels 12; Gaps 3;  
 QY 171 TKCGID-----VTVDKT-----HTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEV 219  
 Db 80 TYTCNVDHKPSNTKVDKTVKRCCEPCPCAPP-VAGPSVFLFPPKPKDTLMISRTPEV 138

QY 220 TCWVDVSHEDPEVKFNWVVDGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKKEY 279  
 Db 139 TCWVDVSHEDPEVFNWVVDGVEVHNATKPREBQFNSTFRVSVLTVLHODWLNKKEY 198  
 QY 280 KCKVSNKALPAPIETKISKAKQPREPQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAV 339  
 Db 199 KCKVSNKGLPAPIETKISKTKQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAV 258  
 QY 340 EWESNGQPNNTKTPPVLDSDGSPFLYSKLTVDKSRWQQQGNVFCVSMHEALHNHYTQK 399  
 Db 259 EWESNGQPNNTKTPPMLDSDGSPFLYSKLTVDKSRWQQQGNVFCVSMHEALHNHYTQK 318  
 QY 400 SLSLSPG 406  
 Db 319 SLSLSPG 325  
 RESULT 8  
 G4HU  
 Ig gamma-4 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
 C:Accession: A90933; A90249; A02150  
 R:Billison, J.; Buxbaum, J.; Hood, L.  
 DNA 1, 11-18, 1981  
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
 A:Reference number: A90933; MUID:83157104; PMID:6299662  
 A:Accession: A90933  
 A:Molecule type: DNA  
 A:Residues: 1-327 <ELL>  
 A:Cross-references: UNIPROT:P01861  
 A:Note: the sequence was determined from the germline gene  
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
 Biochem. J. 117, 33-47, 1970  
 A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re  
 A:Reference number: A90249; MUID:70207560; PMID:4192699  
 A:Accession: A90249  
 A:Molecule type: protein  
 A:Residues: 1-30; 81-326 <PIN>  
 C:Genetics:  
 A:Gene: GDB:IGHG4  
 A:Cross-references: GDB:119340; OMIM:147130  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 99/1; 111/1; 221/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:99-110/Region: hinge  
 F:134-203/Domain: immunoglobulin homology <IM2>  
 F:240-307/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
 F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 50.18; Score 1138.5; DB 1; Length 327;  
 Best Local Similarity 71.1%; Pred. No. 3.8e-62;  
 Matches 224; Conservative 16; Mismatches 30; Indels 45; Gaps 5;  
 QY 137 APCRKHTN-----CSV-----FGLLLTKGNATHDNCISG 166  
 Db 12 APCSRSTSESTAALGCLVKDYPPEPVTWNSGALTSVHTFPFPAVLQSSGLYSLSVVTV 71  
 QY 167 NSPS-----TKCGID-----VTVDKT-----HTCCPCAPPELLGGPSVFLFPPKPKDTL 211  
 Db 72 PSSSLGKTGYTCNVDHKPSNTKVDKRVESKYGPPCPCAPPELLGGPSVFLFPPKPKDTL 131  
 QY 212 MISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNATKPREQYNSTYRVSVLTVLH 271  
 Db 132 MISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNATKPREQYNSTYRVSVLTVLH 191

Qy 272 DWLNGKEYKCKVSNKALPAPIETKISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKG 331  
 Db 192 DWLNGKEYKCKVSNKGLPSSIEKISKAKQPREPQVYTLPPSQBEEMTKNQVSLTCLVKG 251  
 Qy 332 FYPSDIAVESNGQCPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQGNVPSCSVMHEA 391  
 Db 252 FYPSDIAVESNGQCPENNYKTPPVLDSDGSFPLYSRLTVDKSRWQGNVPSCSVMHEA 311  
 Qy 392 LHNHYTKSLSLSPG 406  
 Db 312 LHNHYTKSLSLSLG 326

RESULT 9  
 G3HUWI  
 IG gamma-3 heavy chain disease proteins - human  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999  
 C;Accession: A90442; A92219; A90198; A93915; A02149  
 R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.  
 Biochemistry 19, 4304-4308, 1980  
 A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-  
 A;Reference number: A90442; MUID:81021548; PMID:6774747  
 A;Contents: heavy chain disease protein Wis  
 A;Accession: A90442  
 A;Molecule type: protein  
 A;Residues: 1-289 <FRA>  
 A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
 A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co-  
 A;Note: the sequence of residues 42-76 was taken from the reference that follows  
 R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.  
 J. Biol. Chem. 252, 883-889, 1977  
 A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
 A;Reference number: A92219; MUID:77118561; PMID:402363  
 A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
 A;Accession: A92219  
 A;Molecule type: protein  
 A;Residues: 12-97 <MIC>  
 A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma-  
 idue segment (12-28)  
 A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter-  
 R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.  
 Biochem. Biophys. Res. Commun. 71, 907-914, 1976  
 A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the  
 A;Reference number: A90198; MUID:77021516; PMID:823945  
 A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues  
 A;Accession: A90198  
 A;Molecule type: protein  
 A;Residues: 59-125, 'EB', 128-226, 228-289 <WOL>  
 A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
 R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;  
 Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
 A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion  
 A;Reference number: A93915; MUID:82247835; PMID:6808505  
 A;Contents: heavy chain disease protein Omn  
 A;Accession: A93915  
 A;Molecule type: mRNA  
 A;Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
 A;Note: a carboxyl-terminal Lys is removed posttranslationally  
 A;Note: this sequence may represent an allelic form or another gamma chain subclass  
 C;Comment: The heavy chain disease protein Wis is shown.  
 C;Genetics:  
 A;Gene: GDB:IGHG3  
 A;Cross-references: GDB:119339; OMIM:147120  
 A;Map position: 14q32.33-14q32.33  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid  
 F;203-270/Domain: immunoglobulin homology <IMM>  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;6/140/Binding site: carbohydrate (Asn) #status experimental

Query Match 49.9% Score 1134.5; DB 1; Length 289;

[illegible]

250 GRIFDIDVENWQKNGQFEFEGNIRI1PFQDQVDGIIYFLISKFSVDKASWQGGGIFQCAVM 309

Matches 170; Conservative 32; Mismatches 40; Indels 12; Gaps 5;

QY 165 SGNSSTQKCGID-----VTVDK---THTCPPCP-APELLG-GPSVFLPPPKPKDTLMIS 214  
Db 23 SLSLSSYTCNVNHPATTTTKVDRVGTGKPPCPICPACGPGPSAFIPPPKPKDTLMIS 82  
QY 215 RPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWL 274  
Db 83 RTPKVCVVVDVSDQEPVQFVSVDGVEVHTAQTAPKBEQFNSTYRVVSVLPIQHODWL 142  
QY 275 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334  
Db 143 NGKEFKCKVNNKDLPAPIETRIISKAKGQPREPQVYTLPPTELSRSKVTLCVLTGFYP 202  
QY 335 SDIAVWESNGQ--PENNYKTPPVLDSGSPFLYSLKLTVDKSRWQGNFVSCSNVHEAL 392  
Db 203 PDIDVWQRNGQPEPGNRYTTPQDDVDGTYFLYSKLAVDKASWQRGDTFOCAVNHVAL 262  
QY 393 HNHYTOKSLSLSPG 406  
Db 263 HNHYTOKSIFKTPG 276

RESULT 14  
G2SP  
Ig gamma-2 chain C region - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004  
C:Accession: A94553; A90352; A90359; A90384; A90385; A02151  
R:Trischmann, T.M.  
Submitted to the Atlas, April 1975  
A:Reference number: A94553  
A:Accession: A94553  
A:Molecule type: protein  
A:Residues: 1-3 <TRI>  
A:Cross-references: UNIPROT:P01862  
R:Birsthein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. An  
A:Reference number: A90352; MUID:71058471; PMID:5538606  
A:Accession: A90352  
A:Molecule type: protein  
A:Residues: 4-68 <BIR>  
R:Turner, K.J.; Cebra, J.J.  
Biochemistry 10, 9-17, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. An  
A:Reference number: A90359; MUID:71058486; PMID:5538616  
A:Accession: A90359  
A:Molecule type: protein  
A:Residues: 69-133;312-329 <TUR>  
R:Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90384; MUID:75036072; PMID:4429665  
A:Accession: A90384  
A:Molecule type: protein  
A:Residues: 134-226 <TRA>  
R:Trischmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90385; MUID:75036073; PMID:4609467  
A:Accession: A90385  
A:Molecule type: protein  
A:Residues: 227-311 <TR2>  
R:Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
A:Reference number: A90354; MUID:71058474; PMID:4922544  
A:Contents: annotation; disulfide bonds  
A:Note: Cys-16 is involved in a heavy-light chain bond  
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:21-81/Domain: immunoglobulin homology <IM1>  
F:135-204/Domain: immunoglobulin homology <IM2>  
F:241-310/Domain: immunoglobulin homology <IM3>  
F:248-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:248-308/Disulfide bonds: #status experimental

Query Match 39.4%; Score 895.5; DB 1; Length 329;  
Best Local Similarity 59.7%; Pred. No. 2.1e-47;  
Matches 173; Conservative 31; Mismatches 56; Indels 29; Gaps 5;

QY 127 GFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTVDKTH-- 184  
Db 61 GLYSLTSMVTVPSSQKATC-----NVAHP-----ASSTK---VDKTVBPIRTP 100  
QY 185 -----TCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 239  
Db 101 ZBPBCTCPKCPPEENLGGPSVFIFPPKPKDTLMISLTPTVTCVVVDVSDQEPVQFTWV 160  
QY 240 DGVVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKA 299  
Db 161 DNKPVGNATKPRVQYNTTFRVESVLPQHODWLGKFKCKVYNKALPAPIETKISKT 220  
QY 300 KQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTPPV 357  
Db 221 KGAPRMPEVYTLPPSRDELTKNSKSVSTCLINFFPADIHVEWASNRVPSVEKEYKNTPI 280  
QY 358 LDSGSPFLYSLKLTVDKSRWQGNFVSCSNVHEALHNHVTOKSLSLSPG 406  
Db 281 EDADGSYFLYSLKLTVDKSAWDQGTVTYTCVWHEALHNHVTOKAISRSPG 329

RESULT 15  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47158  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03778; NID:G433121; PIDN:AAA52216.1; PID:G433122  
C:Genetics:  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMW>

Query Match 39.2%; Score 891.5; DB 2; Length 328;  
Best Local Similarity 59.7%; Pred. No. 3.6e-47;  
Matches 172; Conservative 34; Mismatches 57; Indels 25; Gaps 4;

QY 125 PDGPFNSNETSSKAPC-----RKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTV 180  
Db 59 PSGLYSLSMVTVPASSLSKSYTCNV-----NHPATTTKVKRKGVI 100  
QY 181 DKHTTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240  
Db 101 HQPQICPICPGCE--VAGPSVFIFPPKPKDTLMISQTPETVTCVVVDVSKHAEVQFWSYVD 159  
QY 241 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKA 300  
Db 160 GVEVHTAETPRKEQFNSTYRVVSVLPQHODWLGKFKCKVNNVNDLPAPITRTISKAI 219  
QY 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTPPV 358

Db 220 GOSREFQYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTVRTTTPQ 279  
QY 359 DSDGSFFLYSKLTVDKSRWQGNVFSQVMHEALHNHYTKSLSPG 406  
Db 280 DVDGTFFLYSKLAVDKARWDHGDKECAVMHEALHNHYTKSLSKTOG 327

Search completed: March 8, 2005, 14:46:14  
Job time : 17.5467 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 75.0656 Seconds

(without alignments)  
2769.633 Million cell updates/sec

Title: US-09-389-782A-6

Perfect score: 2274

Sequence: 1 ETPPPKYLHYDRETSQILLC.....VMHEALHNHYTQKSLSPG 406

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1231	54.1	330	1 GC1_HUMAN	P01857 homo sapien
2	1231	54.1	465	2 Q6GMX6	Q6gm66 homo sapien
3	1231	54.1	466	2 Q6IN78	Q6in78 homo sapien
4	1231	54.1	469	2 Q7Z7P5	Q7z7p5 homo sapien
5	1231	54.1	470	2 Q6PJA4	Q6pj44 homo sapien
6	1231	54.1	470	2 Q7Z5W1	Q7z5w1 homo sapien
7	1231	54.1	472	2 Q6N089	Q6n089 homo sapien
8	1231	54.1	475	2 Q6GMW7	Q6gmw7 homo sapien
9	1231	54.1	476	2 Q6GMX1	Q6gm67 homo sapien
10	1228	54.0	679	2 Q96PQ8	Q96pq8 homo sapien
11	1227	54.0	473	2 Q6P055	Q6p055 homo sapien
12	1227	54.0	475	2 Q6MZQ6	Q6mzq6 homo sapien
13	1227	54.0	480	2 Q6N094	Q6n094 homo sapien
14	1227	54.0	481	2 Q6N097	Q6n097 homo sapien
15	1227	54.0	482	2 Q7Z351	Q7z351 homo sapien
16	1225	53.9	348	2 Q6PXY1	Q6pxy1 homo sapien
17	1225	53.9	473	2 Q6MZV7	Q6mzv7 homo sapien
18	1225	53.9	478	2 Q6P181	Q6p181 homo sapien
19	1225	53.9	480	2 Q6PJF1	Q6pjf1 homo sapien
20	1225	53.9	544	2 Q6P095	Q6p095 homo sapien
21	1224	53.8	466	2 Q6N096	Q6n096 homo sapien
22	1220	53.6	475	2 Q6N095	Q6n095 homo sapien
23	1211	53.3	487	2 Q652L2	Q652l2 mus sp. fv/
24	1156	50.8	354	2 Q86T72	Q86tt2 homo sapien
25	1154	50.7	518	2 Q6N030	Q6n030 homo sapien
26	1152	50.7	521	2 Q8N4Y9	Q8n4y9 homo sapien
27	1148	50.5	326	1 GC2_HUMAN	P01859 homo sapien
28	1148	50.5	417	2 Q6N093	Q6n093 homo sapien
29	1147	50.4	464	2 Q6MZU6	Q6mzu6 homo sapien
30	1146	50.4	509	2 Q8NF17	Q8nf17 homo sapien
31	1143	50.3	465	2 Q6P6C4	Q6p6c4 homo sapien

32	1138.5	50.1	327	1 GC4_HUMAN	P01861 homo sapien
33	1138.5	50.1	473	2 Q8TC63	Q8tc63 homo sapien
34	1134.5	49.9	290	1 GC3_HUMAN	P01860 homo sapien
35	1134	49.9	493	2 Q68CN4	Q68cn4 homo sapien
36	1130.5	49.7	476	2 Q6MZX7	Q6mzx7 homo sapien
37	1043	45.9	401	1 T11B_HUMAN	O00300 homo sapien
38	926.5	40.7	401	2 Q6P1I2	Q6p1i2 mus musculus
39	922.5	40.6	401	1 T11B_MOUSE	O08712 mus musculus
40	917	40.3	323	1 GC_RABIT	P01870 coryctolagus
41	909	40.0	401	1 T11B_RAT	O08727 rattus norv
42	906	39.8	337	2 Q95M34	Q95m34 equus caball
43	895.5	39.4	329	1 GC2_CAVPO	P01862 cavia porce
44	851	37.4	470	2 Q7TMK1	Q7tmk1 mus musculus
45	848.5	37.3	329	1 GC3_MOUSE	P22436 mus musculus

#### ALIGNMENTS

RESULT 1

GC1_HUMAN	STANDARD;	PRT;	330 AA.
ID GC1_HUMAN			
AC P01857;			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, Last sequence update)			
DT 23-OCT-2004 (Rel. 45, Last annotation update)			
DE 1g gamma-1 chain C region.			
GN Name=IGHG1;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=82274238; PubMed=6287432;			
RA Ellison J.W., Berson B.J., Hood L.E.;			
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL Nucleic Acids Res. 10:4071-4079(1982).			
RN [2]			
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX MEDLINE=71064024; PubMed=5489771;			
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA Waxdal M.J., Edelman G.M.;			
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL Biochemistry 9:3161-3170(1970).			
RN [3]			
RP SEQUENCE OF 136-329 (EU).			
RX MEDLINE=71064025; PubMed=5530842;			
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA Edelman G.M.;			
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL Biochemistry 9:3171-3181(1970).			
RN [4]			
RP SEQUENCE (MYELOMA PROTEIN NIE).			
RX MEDLINE=77070269; PubMed=826475;			
RA Ponstingl H., Hilschmann N.;			
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";			
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN [5]			
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX MEDLINE=83289131; PubMed=6884994;			
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN [6]			
RP DISULFIDE BONDS.			
RX MEDLINE=71064027; PubMed=4923144;			

RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RN Biochemistry 9:3188-3196(1970).  
 RP [7]  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from *Staphylococcus*  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC GIM(3) marker and the GIM (non-1) markers.  
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; J00228; AAC92527.1; ALT\_INIT.  
 DR PIR; A93433; GHU.  
 DR PDB; 1A77; X-ray; H=1-103.  
 DR PDB; 1DSB; X-ray; B/H=1-101.  
 DR PDB; 1DSI; X-ray; H=1-101.  
 DR PDB; 1DSV; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1E4K; X-ray; A/B=106-329.  
 DR PDB; 1FC1; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FCC; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I7Z; X-ray; B/D=1-103.  
 DR PDB; 1IIS; X-ray; A/B=107-330.  
 DR PDB; 1IIX; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1LQX; X-ray; A/B=119-330.  
 DR PDB; 2RCS; X-ray; H=1-103.  
 DR Genew; HGNC:5525; IGHG1.  
 DR MiM; 147100; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW Immunoglobulin C region; Immunoglobulin domain.  
 FT NON TER 1 98 CH1.  
 FT DOMAIN 99 110 Hinge.  
 FT

FT DOMAIN 111 223  
 FT DOMAIN 224 330  
 FT DISULFID 27 83  
 FT DISULFID 103 103  
 FT DISULFID 109 109  
 FT DISULFID 112 112  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT CARBOHYD 180 180  
 FT VARIANT 97 97  
 FT VARIANT 239 239  
 FT VARIANT 241 241  
 FT STRAND 23 24  
 FT STRAND 26 33  
 FT STRAND 38 38  
 FT STRAND 41 41  
 FT TURN 42 45  
 FT TURN 48 49  
 FT STRAND 50 52  
 FT STRAND 57 58  
 FT STRAND 59 61  
 FT STRAND 62 71  
 FT HELIX 73 75  
 FT TURN 76 78  
 FT STRAND 82 87  
 FT TURN 88 91  
 FT STRAND 92 97  
 FT TURN 102 103  
 FT STRAND 122 126  
 FT HELIX 130 134  
 FT TURN 136 137  
 FT STRAND 141 149  
 FT STRAND 157 162  
 FT TURN 163 164  
 FT STRAND 165 167  
 FT STRAND 171 172  
 FT STRAND 176 177  
 FT TURN 179 180  
 FT STRAND 183 190  
 FT HELIX 193 197  
 FT TURN 198 199  
 FT STRAND 202 207  
 FT TURN 209 210  
 FT STRAND 215 219  
 FT STRAND 227 227  
 FT STRAND 230 234  
 FT HELIX 238 242  
 FT STRAND 245 256  
 FT STRAND 261 266  
 FT TURN 267 268  
 FT STRAND 269 270  
 FT STRAND 274 276  
 FT TURN 280 281  
 FT TURN 283 284  
 FT STRAND 287 296  
 FT HELIX 297 301  
 FT TURN 302 303  
 FT STRAND 306 311  
 FT TURN 313 314  
 FT HELIX 316 318  
 FT STRAND 319 324  
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 54.1%; Score 1231; DB 1; Length 330;  
 Best Local Similarity 92.5%; Pred. No. 1.4e-72;  
 Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;

Oy 159 TDNICSGNSE-STQKCGIDV---TVDKTHTCPCPAPELLGGPSVFLPDKPTLMIS 214  
 Db 78 TQTVICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPDKPTLMIS 137

QY 215 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274  
 DB 138 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 197  
 QY 275 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYP 334  
 DB 198 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYP 257  
 QY 335 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 394  
 DB 258 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 317  
 QY 395 HYTKQSLSLSPG 406  
 DB 318 HYTKQSLSLSPG 329

RESULT 2  
 Q6GMX6 PRELIMINARY; PRT; 465 AA.

AC Q6GMX6  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Casavant T.L., Scheetz T.E.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766; AAH73766.1; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IG; 1.  
 DR SMART; SM00407; IG; 3.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.

SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;  
 Query Match 54.1%; Score 1231; DB 2; Length 465;  
 Best Local Similarity 92.5%; Pred. No. 2.1e-72;  
 Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;

QY 159 THDNICGNSH-STQKCGIDV---TVDKTHTCPCPAPELGPGSVFLPPPKDPTLMIS 214  
 DB 213 TQTYICNVNHNKTSNTKVDKVKVPKSCDKTHTCPCPAPELGPGSVFLPPPKDPTLMIS 272  
 QY 215 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274  
 DB 273 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 332  
 QY 275 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYP 334  
 DB 333 NGKEYKCKVSNKALPAPIETKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYP 392  
 QY 335 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 394  
 DB 393 SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHN 452  
 QY 395 HYTKQSLSLSPG 406  
 DB 453 HYTKQSLSLSPG 464

RESULT 3  
 Q6IN78 PRELIMINARY; PRT; 466 AA.

AC Q6IN78  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE IGHG1 protein.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC072419; AAH72419.1; -;  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.



RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018747; AAH18747.1; -  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;  
  
Query Match 54.1%; Score 1231; DB 2; Length 470;  
Best Local Similarity 92.5%; Pred. No. 2.1e-72;  
Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;  
  
QY 159 THDNICGNSG-STQKCGIDV---TVDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 214  
DB 218 TQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 277  
  
QY 215 RPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274  
DB 278 RPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 337  
  
QY 275 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334  
DB 338 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397  
  
QY 335 SDIAVESWGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 394  
DB 398 SDIAVESWGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 457  
  
QY 395 HYTKSLSLSPG 406  
DB 458 HYTKSLSLSPG 469  
  
RESULT 6  
Q725W1 PRELIMINARY; PRT; 470 AA.  
AC Q725W1  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Cunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAH53984.1; -  
DR HSSP; P01857; IHZH.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;  
  
Query Match 54.1%; Score 1231; DB 2; Length 470;  
Best Local Similarity 92.5%; Pred. No. 2.1e-72;  
Matches 233; Conservative 3; Mismatches 12; Indels 4; Gaps 2;  
  
QY 159 THDNICGNSG-STQKCGIDV---TVDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 214  
DB 218 TQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMIS 277  
  
QY 215 RPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274  
DB 278 RPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 337  
  
QY 275 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334  
DB 338 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 397  
  
QY 335 SDIAVESWGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 394  
DB 398 SDIAVESWGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHN 457  
  
QY 395 HYTKSLSLSPG 406  
DB 458 HYTKSLSLSPG 469  
  
RESULT 7  
Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686P15220.  
GN Name=DKFZp686P15220;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;





Q6P055 PRELIMINARY; PRT; 473 AA.

AC Q6P055; 401 SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSVMEGLHN 460

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral Nervous System;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalak U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral Nervous System;

RA Strausberg R.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC065820; AAH65820.1; -.

DR HSSP; P01861; IADQ.

DR InterPro; IPR003559; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG.cl.

DR InterPro; IPR003006; IG.MHC.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 4.

DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.

KW Hypothetical protein.

SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129857 CRC64;

Query Match 54.0%; Score 1227; DB 2; Length 473;

Best Local Similarity 92.1%; Pred. No. 3.9e-72;

Matches 232; Conservative 3; Mismatches 13; Indels 4; Gaps 2;

QY 159 THDNICSGNSE-STOKCGIDV---TVDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMIS 214

DB 221 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPAPPELLGGPSVFLFPPKPKDTLMIS 280

QY 215 RTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274

DB 281 RTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 340

QY 275 NGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334

DB 341 NGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 400

QY 335 SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSVMEGLHN 394

DB 401 SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSVMEGLHN 460

QY 395 HYTKSLSLSPG 406

DB 461 HYTKSLSLSPG 472

RESULT 12

Q6MZQ6 PRELIMINARY; PRT; 475 AA.

ID Q6MZQ6;

AC Q6MZQ6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein DXFZp686G11190.

GN Name=DXFZp686G11190;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Human esophagus tumor;

RG The German Human CDNA Consortium;

RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,

RA Han M., Wiemann S.;

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640947; CAE45972.1; -.

DR HSSP; P01861; IADQ.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG.cl.

DR InterPro; IPR003006; IG.MHC.

DR InterPro; IPR003596; IG.v.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 4.

DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.

KW Hypothetical protein.

SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 54.0%; Score 1227; DB 2; Length 475;

Best Local Similarity 92.1%; Pred. No. 3.9e-72;

Matches 232; Conservative 3; Mismatches 13; Indels 4; Gaps 2;

QY 159 THDNICSGNSE-STOKCGIDV---TVDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMIS 214

DB 223 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTCPAPPELLGGPSVFLFPPKPKDTLMIS 282

QY 215 RTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 274

DB 283 RTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL 342

QY 275 NGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 334

DB 343 NGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP 402

QY 335 SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSVMEGLHN 394

DB 403 SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSVMEGLHN 462

QY 395 HYTKSLSLSPG 406

DB 463 HYTKSLSLSPG 474

RESULT 13

Q6N094 PRELIMINARY; PRT; 480 AA.

ID Q6N094

AC Q6N094;





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 84.7356 Seconds  
(without alignments)  
1843.986 Million cell updates/sec

Title: US-09-389-782A-7  
Perfect score: 2264  
Sequence: 1 ETFPPKYLHYDRETSQLLC.....VMHEALHNYTKSLSPG 404

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp19808:.\*  
2: Geneseqp19908:.\*  
3: Geneseqp20008:.\*  
4: Geneseqp20018:.\*  
5: Geneseqp20028:.\*  
6: Geneseqp20038:.\*  
7: Geneseqp20038b:.\*  
8: Geneseqp20048:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2264	100.0	404	AAB80903	Human OPG
2	2264	100.0	404	AAY72921	Human OPG
3	2199	97.1	425	ABG71831	Human OPG
4	2192.5	96.8	413	AAB80900	Human OPG
5	2192.5	96.8	413	AAY72918	Human ost
6	2191.5	96.8	407	AAB80899	Human OPG
7	2191.5	96.8	407	AAY72917	Human ost
8	2191	96.8	400	AAB80901	Human OPG
9	2191	96.8	400	AAY72919	Human OPG
10	2191	96.8	406	AAB80902	Human OPG
11	2191	96.8	406	AAY72920	Human OPG
12	2191	96.8	422	AAB66993	OPG-Fc. 4
13	1501.5	66.3	659	ABJ37103	Concatame
14	1501.5	66.3	659	ADQ79910	Human tum
15	1496.5	66.1	450	ADL06639	stnFRII:1
16	1496	66.1	489	ADM32913	Amino aci
17	1493.5	66.0	490	ABJ37099	Concatame
18	1493.5	66.0	490	ADQ79902	Human tum
19	1493.5	66.0	720	ABJ37101	Concatame
20	1493.5	66.0	720	ADQ79906	Human tum
21	1481	65.4	518	AAB50080	TNFR:Fc f
22	1481	65.4	518	AAB70001	stnFR (075
23	1467	64.8	518	AAr51003	Sequence
24	1460	64.5	485	AAr24016	Fusion pr
25	1436.5	63.4	444	ABG71833	RANK bind

26	1435.5	63.4	443	6	ABP58181	Human RAN
27	1435.5	63.4	443	6	AAE34361	Human RAN
28	1430.5	63.2	440	7	ADJ66000	Herpes v1
29	1430.5	63.2	440	8	ADP03589	Infection
30	1422	62.8	439	8	ADO47876	Alpha-Her
31	1396.5	61.7	442	7	ADB17002	Human RAN
32	1396.5	61.7	443	7	ADB17001	Human RAN
33	1393	61.5	443	7	ADB17000	Murine RA
34	1361.5	60.1	608	6	ABJ37102	Concatame
35	1361.5	60.1	608	8	ADQ79908	Human tum
36	1353.5	59.8	444	6	ABJ37098	Concatame
37	1353.5	59.8	444	8	ADQ79900	Human tum
38	1353.5	59.8	628	6	ABJ37100	Concatame
39	1353.5	59.8	628	8	ADQ79904	Human tum
40	1344.5	59.4	445	7	ADL06637	stnFRI:19
41	1332	58.8	376	2	AAW60037	Antigenic
42	1325.5	58.5	396	8	ADF57557	Mouse ymk
43	1324.5	58.5	398	7	ABW02717	Mouse tms
44	1324.5	58.5	398	8	ADJ45758	Murine tm
45	1317	58.2	376	2	AAW50287	Human Fas

ALIGNMENTS

RESULT 1  
AAB80903  
ID AAB80903 standard; protein; 404 AA.  
XX  
AC AAB80903;  
XX  
DT 31-MAY-2001 (first entry)  
XX  
DE Human OPG(22-194)-FcG10 fusion protein.  
XX  
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;  
KW osteoclast formation inhibition; bone resorption inhibition;  
KW immunoglobulin.  
XX  
OS Homo sapiens.  
XX  
PN WO200117543-A2.  
XX  
PD 15-MAR-2001.  
XX  
PF 18-AUG-2000; 2000WO-US022806.  
XX  
PR 03-SEP-1999; 99US-00389545.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Dunstan CR;  
XX  
DR WPI; 2001-265936/27.  
XX  
PT Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegrin polypeptide.  
XX  
PS Disclosure; Fig 7; 87pp; English.

The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic

CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
 CC or treatment of loss of bone mass, which occurs in conditions including  
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating  
 CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and  
 CC CH3 regions; see AAB80897-8)  
 XX  
 SQ Sequence 404 AA;

Query Match 100.0%; Score 2264; DB 4; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-133;  
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETPPPKYLHYDEETSHQLLCKDCPPGYLKQCTAKWTKVPCAPCPDHYVYDTSWHTSDECL 60  
 Db 1 ETPPPKYLHYDEETSHQLLCKDCPPGYLKQCTAKWTKVPCAPCPDHYVYDTSWHTSDECL 60  
 QY 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPGFGVVOAGTTPERNTV 120  
 Db 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPGFGVVOAGTTPERNTV 120  
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180  
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180  
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180  
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180  
 QY 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240  
 Db 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240  
 QY 241 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 300  
 Db 241 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 300  
 QY 301 PREPQYVITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDG 360  
 Db 301 PREPQYVITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDG 360  
 QY 361 SPFLYSKLTVDKSRWQQGNVFCSVWHEALHNHYTQKSLSLSPG 404  
 Db 361 SPFLYSKLTVDKSRWQQGNVFCSVWHEALHNHYTQKSLSLSPG 404

RESULT 2

AAY72921

ID AAY72921 standard; protein; 404 AA.

XX

AC AAY72921;

XX

DT 13-JUN-2001 (first entry)

XX

DE Human OPG (22-194 residues) -FcG10 fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 KW periodontal.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..173  
 FT /note= "Derived from human osteoprotegerin fragment (22-  
 FT 194 residues)"  
 FT Region 174..182  
 FT /label= Ser- (Gly) 8 linker  
 FT Region 183..404  
 FT /note= Corresponds to 10-231 residues of human IgG1 Fc  
 FT region  
 XX WO200118203-A1.  
 PN 15-MAR-2001.  
 XX 18-AUG-2000; 2000WO-US022797.  
 XX 03-SEP-1999; 99US-00389782.  
 XX (AMGE-) AMGEN INC.  
 XX Dunstan CR, Wooden SK, Mann MB;  
 XX WPI; 2001-244572/25.  
 DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
 PT by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 XX Claim 7; Fig 7; 119pp; English.  
 XX The present sequence is a fusion protein comprising a sequence derived  
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with  
 CC human immunoglobulin G1 (IgG1) FcG10 region (lacks 1-9 residues and has a  
 CC Ser- (Gly) 8 linker). OPG negatively regulates the formation of osteoclasts  
 CC in vitro and in vivo. It blocks the differentiation of osteoclasts from  
 CC monocyte or macrophage precursors and the reabsorption of bone. The OPG-  
 CC Fc fusion protein is administered for the treatment of bone loss  
 CC resulting from osteoporosis, Paget's disease, osteomyelitis,  
 CC hypercalcaemia, osteopenia associated with surgery or steroid  
 CC administration, osteonecrosis, bone loss due to rheumatoid arthritis,  
 CC periodontal bone loss, osteolytic metastasis and/or prosthetic loosening  
 XX  
 SQ Sequence 404 AA;  
 Query Match 100.0%; Score 2264; DB 4; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-133;  
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ETPPPKYLHYDEETSHQLLCKDCPPGYLKQCTAKWTKVPCAPCPDHYVYDTSWHTSDECL 60  
 Db 1 ETPPPKYLHYDEETSHQLLCKDCPPGYLKQCTAKWTKVPCAPCPDHYVYDTSWHTSDECL 60  
 QY 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPGFGVVOAGTTPERNTV 120  
 Db 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPGFGVVOAGTTPERNTV 120  
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180  
 Db 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKSGGGGG 180  
 QY 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240  
 Db 181 GGTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 240  
 QY 241 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 300

Db 241 EVHNAKTKPREQYNSYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQ 300  
QY 301 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPNYKTTTPVLDSDG 360  
Db 301 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPNYKTTTPVLDSDG 360  
QY 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 404  
Db 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 404

## RESULT 3

ABG71831  
ID ABG71831 standard; protein; 425 AA.

XX AC ABG71831;

XX DT 14-APR-2003 (first entry)

XX DE Human OPG protein for expression in mammalian cells.

XX KW RANKL; human receptor activator of NfkappaB; osteoprotegerin; OPG;

XX KW RANKL ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;

XX KW osteoporosis; bone disease; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200264782-A2.

XX PD 22-AUG-2002.

XX PF 08-FEB-2002; 2002WO-000090.

XX PR 09-FEB-2001; 2001DK-00000214.

XX PR 09-FEB-2001; 2001US-0267843P.

XX PR 23-MAR-2001; 2001DK-00000498.

XX PR 23-MAR-2001; 2001US-0278320P.

XX PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX PI Haaning JM, Halkier T;

XX DR WPI; 2002-691592/74.

XX DR N-PSDB; ABS56347.

XX PT Novel human receptor activator of NfkappaB (hRANK) or human

XX PT osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand

XX PT (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for

XX PT treating osteoporosis.

XX PS Example 4; Fig 12; 129pp; English.

XX CC This invention relates to a novel polypeptide having an amino acid  
CC sequence that is different from and is at least about 70% identical to  
CC the amino acid sequence of human receptor activator of NfkappaB (hRANK)  
CC or human osteoprotegerin (hOPG), and which has a binding affinity to RANK  
CC ligand (RANKL) that is at least as high as the binding affinity of hRANK  
CC or hOPG to RANKL, as determined by functional competition assay. The  
CC protein of the invention may have osteopathic activity and may act as a  
CC RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity  
CC inhibitor. The nucleotide sequence shown in the invention may be used in  
CC gene therapy. The protein of the invention or fusion proteins comprising  
CC this protein are useful as a pharmaceutical, and in the preparation of a  
CC medicament for treating or preventing osteoporosis, or other bone  
CC diseases or diseases associated with binding of RANKL to the RANK  
CC receptor. A host cell containing a vector expressing the protein is  
CC useful for producing a polypeptide having binding affinity to RANKL,  
CC where the polypeptide comprises at least one N- or O-glycosylation site  
CC and the host cell is a eukaryotic host cell capable of in vivo  
CC glycosylation, and/or the polypeptide is subjected to conjugation to a  
CC non-polypeptide moiety in vitro. The protein of the invention has

CC increased functional in vivo half-life and/or serum half-life compared to  
CC hRANK or hOPG and has an improved binding affinity to RANKL compared to  
CC the binding affinity of hRANK or hOPG to RANKL, as determined by a  
CC functional competition assay. The present sequence represents a human OPG  
CC protein modified for expression in a mammalian system, this sequence has  
CC the human OPG protein fused to a Leu-Glu dipeptide and amino acid  
CC residues 247-475 of human IgG1

XX SQ Sequence 425 AA;

Query Match 97.1%; Score 2199; DB 5; Length 425;  
Best Local Similarity 97.8%; Pred. No. 3.9e-129;  
Matches 395; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDETSQQLCDKPPGTYLKQHTAKWTKVPCAPCPHYHYTDSWHTSDECL 60

Db 22 ETFPKYLHYDETSQQLCDKPPGTYLKQHTAKWTKVPCAPCPHYHYTDSWHTSDECL 81

QY 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVQAGTTPERTV 120

Db 82 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCTPPGFGVVQAGTTPERTV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSBSTQKSGGGGG 180

Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSBSTQKSGGGGG 201

QY 181 GGTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV 240

Db 202 THTCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV 261

QY 241 EVHNAKTKPREQYNSYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQ 300

Db 262 EVHNAKTKPREQYNSYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQ 321

QY 301 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPNYKTTTPVLDSDG 360

Db 322 PREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPNYKTTTPVLDSDG 381

QY 361 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 404

Db 382 SPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPG 425

## RESULT 4

AAB80900

ID AAB80900 standard; protein; 413 AA.

XX AC AAB80900;

XX DT 31-MAY-2001 (first entry)

XX DE Human OPG(22-201)-Fc fusion protein.

XX KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;

XX KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;

XX KW osteoclast formation inhibition; bone resorption inhibition;

XX KW immunoglobulin.

XX OS Homo sapiens.

XX PN WO200117543-A2.

XX PD 15-MAR-2001.

XX PF 18-AUG-2000; 2000WO-US022806.

XX PR 03-SEP-1999; 99US-00389545.

XX PA (AMGE-) AMGEN INC.

XX PI Dunstan CR;

XX DR WPI; 2001-265936/27.

XX Preventing or treating lytic bone diseases, particularly associated with  
PT cancer or metastasis, by administering an osteoprotegerin polypeptide.  
XX  
XX Disclosure; Fig 4; 87pp; English.  
XX  
XX The present invention relates to a method for the prevention or treatment  
CC of lytic bone disease or multiple myeloma. Also the method can be used  
CC for preventing metastasis of cancer to bone or osteosclerotic bone  
CC metastasis. The method comprises administering an OPG (osteoprotegerin)  
CC polypeptide or OPG fusion protein. The present sequence is one such OPG  
CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone  
CC resorption) by blocking differentiation from monocytes/macrophage  
CC precursors. The OPG polypeptide can be used in a method of preventing or  
CC treating lytic bone disease, for preventing metastasis of cancer to bone  
CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal  
CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic  
CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
CC or treatment of loss of bone mass, which occurs in conditions including  
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
CC congenital forms of osteoporosis (osteogenesis imperfecta,  
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
CC leukaemia); idiopathic hypercalcaemia, and hypercalcaemia associated with  
CC hyperthyroidism and renal function disorders; osteopaenia following  
CC surgery, induced by steroid administration, and associated with disorders  
CC of the small and large intestine and with chronic hepatic and renal  
CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
CC are also used in the replacement of structurally sound bone with  
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
CC in adults and juveniles; hyperparathyroidism, in congenital bone  
CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
CC metastases. The OPG fusion proteins can exhibit increased circulating  
CC half-lives and slower clearance times, thereby providing a more sustained  
CC activity. The OPG fusion protein comprises a fragment of the human OPG  
CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and  
CC CH3 regions; see AAB80897-8)  
XX  
XX Sequence 413 AA;

Query Match 96.8%; Score 2192.5; DB 4; Length 413;  
Best Local Similarity 95.9%; Pred. No. 9,6e-129;  
Matches 396; Conservative 0; Mismatches 8; Indels 9; Gaps 1;

QY 1 ETFPKKYLYHDETSKQCDKCPGTYLKHCHTAKWTKVCAPCDPHYVYDSWHTSDECL 60  
Db 1 ETFPKKYLYHDETSKQCDKCPGTYLKHCHTAKWTKVCAPCDPHYVYDSWHTSDECL 60  
QY 61 YCSPVCKELQYVKQECNTRHNRCVCEKGRYLEIEFCLKHSRCPGFGVQAGTPTERTV 120  
Db 61 YCSPVCKELQYVKQECNTRHNRCVCEKGRYLEIEFCLKHSRCPGFGVQAGTPTERTV 120  
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGNSSTQKSGGGGG 180  
Db 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSGNSSTQKSGGGGG 180  
QY 181 GG-----TCPPCPAPELGGSVFLFPKPKDXTLMISRTPEVTCVVDVSHEDPEV 231  
Db 181 AAPKSCDKTHTCPPCPAPELGGSVFLFPKPKDXTLMISRTPEVTCVVDVSHEDPEV 240  
QY 232 KFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIE 291  
Db 241 KFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIE 300

QY 292 KTIISKAKGQPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 351  
Db 301 KTIISKAKGQPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 360  
QY 352 TTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNNHYTKQSLSLSPG 404  
Db 361 TTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNNHYTKQSLSLSPG 413  
RESULT 5  
AA72918  
ID AAY72918 standard; protein; 413 AA.  
XX  
AC AAY72918;  
DT 13-JUN-2001 (first entry)  
XX  
DE Human osteoprotegerin (22-201 residues)-IgG1 Fc region fusion protein.  
XX  
KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
KW periodontal.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..179  
FT /note= "derived from human osteoprotegerin fragment (22-  
FT 201 residues)"  
FT Region 180..182  
FT /label= Linker  
FT Region 183..413  
FT /label= Human\_IgG1\_Fc\_region  
XX  
PN WO200118203-A1.  
XX  
PD 15-MAR-2001.  
XX  
PF 18-AUG-2000; 2000WO-US022797.  
XX  
PR 03-SEP-1999; 99US-00389782.  
XX (AMGE-) AMGEN INC.  
XX Dunstan CR, Wooden SK, Mann MB;  
XX  
DR WPI; 2001-244572/25.  
XX  
PT Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
PT by e.g. osteoporosis, Paget's disease and osteomyelitis.  
XX  
PS Example 1; Fig 4; 119pp; English.  
XX  
CC The present sequence is a fusion protein comprising a sequence derived  
CC from human osteoprotegerin (OPG; 22-201 residues) which is fused with  
CC human immunoglobulin G1 (IgG1) Fc region by a linker. OPG negatively  
CC regulates the formation of osteoclasts in vitro and in vivo. It blocks  
CC the differentiation of osteoclasts from monocyte or macrophage precursors  
CC and the reabsorption of bone. The OPG-Fc fusion protein is administered  
CC for the treatment of bone loss resulting from osteoporosis, Paget's  
CC disease, osteomyelitis, hypercalcaemia, osteopenia associated with  
CC surgery or steroid administration, osteonecrosis, bone loss due to  
CC rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or  
CC prosthetic loosening  
XX  
SQ Sequence 413 AA;

Query Match 96.8%; Score 2192.5; DB 4; Length 413;  
Best Local Similarity 95.9%; Pred. No. 9,6e-129;  
Matches 396; Conservative 0; Mismatches 8; Indels 9; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETTPPKYLHYDEETSHQLLCKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKXRSPPGFGVVQAGTPERTV 120  
 DB 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKXRSPPGFGVVQAGTPERTV 120  
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNTCSGNSSTQKSGGGG 180  
 DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNTCSGNSSTQKSGGGG 180  
 QY 181 GG-----TCPPCAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEV 231  
 DB 181 AAPKSCDKTHTCPPCAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEV 240  
 QY 232 KFNWYDGVVHNKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 291  
 DB 241 KFNWYDGVVHNKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 300  
 QY 292 KTISKAKQPRBQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 351  
 DB 301 KTISKAKQPRBQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 360  
 QY 352 TTPVLSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 404  
 DB 361 TTPVLSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 413

## RESULT 6

AAB80899  
 ID AAB80899 standard; protein; 407 AA.

XX AAB80899;  
 XX AC  
 XX 31-MAY-2001 (first entry)  
 XX Human OPG(22-194)-Fc fusion protein.

XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;  
 KW osteoclast formation inhibition; bone resorption inhibition;  
 KW immunoglobulin.

XX Homo sapiens.  
 XX WO200117543-A2.  
 XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.

XX (AMGE-) AMGEN INC.

XX Dunstan CR;

XX WPI; 2001-265936/27.

XX Preventing or treating lytic bone diseases, particularly associated with  
 PT cancer or metastasis, by administering an osteoprotegrin polypeptide.

XX Disclosure; Fig 3; 87pp; English.

XX The present invention relates to a method for the prevention or treatment  
 CC of lytic bone disease or multiple myeloma. Also the method can be used  
 CC for preventing metastasis of cancer to bone or osteosclerotic bone  
 CC metastasis. The method comprises administering an OPG (osteoprotegrin)  
 CC polypeptide or OPG fusion protein. The present sequence is one such OPG  
 CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone  
 CC resorption) by blocking differentiation from monocytes/macrophage  
 CC precursors. The OPG polypeptide can be used in a method of preventing or

CC treating lytic bone disease, for preventing metastasis of cancer to bone  
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal  
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic  
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
 CC or treatment of loss of bone mass, which occurs in conditions including  
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating  
 CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and  
 CC CH3 regions; see AAB80897-8)

XX SQ Sequence 407 AA;

Query Match 96.8%; Score 2191.5; DB 4; Length 407;  
 Best Local Similarity 97.1%; Pred. No. 1.1e-128;  
 Matches 395; Conservative 1; Mismatches 8; Indels 3; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETTPPKYLHYDEETSHQLLCKPPGTYLKQHCCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKXRSPPGFGVVQAGTPERTV 120  
 DB 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLIEFCLKXRSPPGFGVVQAGTPERTV 120  
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNTCSGNSSTQKSGG--G 177  
 DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNTCSGNSSTQKAAEPPKS 180  
 QY 178 GGGGGTCCPPCAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 237  
 DB 181 CDKTHTCPPCAPPELLGSPVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 240  
 QY 238 DGVVHNKTKPREBQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 297  
 DB 241 DGVVHNKTKPREBQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 300  
 QY 298 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLVD 357  
 DB 301 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLVD 360  
 QY 358 SDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 404  
 DB 361 SDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 407

## RESULT 7

AAY72917  
 ID AAY72917 standard; protein; 407 AA.

XX AAY72917;

```

XX DT 13-JUN-2001 (first entry)
XX DE Human osteoprotegerin (22-194 residues) - IgG1 Fc region fusion protein.
XX KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
XX KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
XX KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
XX KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
XX KW periodontal.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT Region 1. .173
XX FT /note= "Derived from human osteoprotegerin fragment (22-
XX FT 194 residues)"
XX FT Region 174. .176
XX FT /label= Linker
XX FT Region 177. .407
XX FT /label= Human_IgG1_Fc_region
XX WO200118203-A1.
XX PN 15-MAR-2001.
XX PD 18-AUG-2000; 2000WO-US022797.
XX PF 03-SEP-1999; 99US-00389782.
XX PR (AMGE-) AMGEN INC.
XX PA Dunstan CR, Mann MB;
XX PI WPI; 2001-244572/25.
XX DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
XX PT by e.g. osteoporosis, Paget's disease and osteomyelitis.
XX PS Example 1; Fig 3; 119pp; English.
XX CC The present sequence is a fusion protein comprising a sequence derived
XX CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with
XX CC human immunoglobulin G1 (IgG1) Fc region by a linker. OPG negatively
XX CC regulates the formation of osteoclasts in vitro and in vivo. It blocks
XX CC the differentiation of osteoclasts from monocyte or macrophage precursors
XX CC and the reabsorption of bone. The OPG-Fc fusion protein is administered
XX CC for the treatment of bone loss resulting from osteoporosis, Paget's
XX CC disease, osteomyelitis, hypercalcaemia, osteopenia associated with
XX CC surgery or steroid administration, osteonecrosis, bone loss due to
XX CC rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or
XX CC prosthetic loosening
XX SQ Sequence 407 AA;
XX Query Match 96.8%; Score 2191.5; DB 4; Length 407;
XX Best Local Similarity 97.1%; Pred. No. 1.1e-128;
XX Matches 395; Conservative 1; Mismatches 8; Indels 3; Gaps 1;
XX
XX 1 ETFFPKYLYHDETSQQLCDKCPGTYLKQKCTAKWTKVCAPCPDHYVTSWHTSDCL 60
XX 1 ETFFPKYLYHDETSQQLCDKCPGTYLKQKCTAKWTKVCAPCPDHYVTSWHTSDCL 60
XX
XX 61 YCSPVCKELQYKQECNRTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNV 120
XX 61 YCSPVCKELQYKQECNRTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNV 120
XX
XX 121 CKRCPDGFPSNETSSKAPCKRHTNCSVFGLLLTQKGNATHNICSGNSETQKSGG---G 177
XX 121 CKRCPDGFPSNETSKAPCKRHTNCSVFGLLLTQKGNATHNICSGNSETQKAAEPKS 180
XX
XX 178 GGGGTCTPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWV 237
XX

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Db 181 CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWV 240
QY 238 DGVEVHNATKPREEQYNSTYRWVSIVTLVHODWLNKKEYCKVSNKALPAPIEKTISKA 297
Db 241 DGVEVHNATKPREEQYNSTYRWVSIVTLVHODWLNKKEYCKVSNKALPAPIEKTISKA 300
QY 298 KQCPREPQVYTLPPSRDELTKQVSLTCLVKGFPDIAVEWESNGQPNNTKTPPVLD 357
Db 301 KQCPREPQVYTLPPSRDELTKQVSLTCLVKGFPDIAVEWESNGQPNNTKTPPVLD 360
QY 358 SDGSFPLYSKLTVDKSRWQQGNVFCVSWHEALHNHYTKSLSPG 404
Db 361 SDGSFPLYSKLTVDKSRWQQGNVFCVSWHEALHNHYTKSLSPG 407

RESULT 8
AAB80901
ID AAB80901 standard; protein; 400 AA.
AC AAB80901;
DT 31-MAY-2001 (first entry)
DE Human OPG(22-194)-FcdeltaC fusion protein.
KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.
OS Homo sapiens.
PN WO200117543-A2.
PD 15-MAR-2001.
PF 18-AUG-2000; 2000WO-US022806.
PR 03-SEP-1999; 99US-00389545.
PA (AMGE-) AMGEN INC.
PI Dunstan CR;
DR WPI; 2001-265936/27.
PT Preventing or treating lytic bone diseases, particularly associated with
XX cancer or metastasis, by administering an osteoprotegrin polypeptide.
PS Claim 11; Fig 5; 87pp; English.
XX
XX The present invention relates to a method for the prevention or treatment
XX of lytic bone disease or multiple myeloma. Also the method can be used
XX for preventing metastasis of cancer to bone or osteosclerotic bone
XX metastasis. The method comprises administering an OPG (osteoprotegrin)
XX polypeptide or OPG fusion protein. The present sequence is one such OPG
XX fusion protein. OPG inhibits formation of osteoclasts (and thus bone
XX resorption) by blocking differentiation from monocytes/macrophage
XX precursors. The OPG polypeptide can be used in a method of preventing or
XX treating lytic bone disease, for preventing metastasis of cancer to bone
XX (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
XX rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
XX tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
XX bone metastasis. The OPG fusion polypeptides are used in the prevention
XX or treatment of loss of bone mass, which occurs in conditions including
XX osteoporosis, such as primary osteoporosis, endocrine osteoporosis
XX (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
XX congenital forms of osteoporosis (osteogenesis imperfecta,
XX homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
XX due to immobilisation of extremities; Paget's disease of bone (osteitis
XX deformans) in adults and juveniles; osteomyelitis, or an infectious
XX lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
XX and kidney) and haematologic malignancies (multiple myeloma, lymphoma and

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CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating  
 CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the FC region of immunoglobulin IgGgamma1 (the hinge, CH2 and  
 CC CH3 regions; see AAB80897-8)  
 XX  
 SQ Sequence 400 AA;

Query Match 96.8%; Score 2191; DB 4; Length 400;  
 Best Local Similarity 97.8%; Pred. No. 1.1e-128;  
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 1 ETTPPKYLHYDEBTSQQLCDKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETTPPKYLHYDEBTSQQLCDKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGFGVWVQAGTPERTV 120  
 DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGFGVWVQAGTPERTV 120  
 QY 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSGSESTOKSGGGGG 180  
 DB 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSGSESTOKV----DK 176  
 QY 181 GGTCPCPAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240  
 DB 177 THTCPCPAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 236  
 QY 241 EVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 300  
 DB 237 EVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 296  
 QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360  
 DB 297 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 356  
 QY 361 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404  
 DB 357 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 400

RESULT 9  
 AAY72919  
 ID AAY72919 standard; protein; 400 AA.  
 XX  
 AC AAY72919;  
 XX  
 DT 13-JUN-2001 (first entry)  
 DE Human OPG (22-194 aa)-Fc region (lacking 1-5 residues) fusion protein.  
 XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 KW periodontal.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers

FT Region 1. .173  
 FT /note= "Derived from human osteoprotegerin fragment (22-  
 FT 174 194 residues)"  
 FT Region 174  
 FT /label= Linker  
 FT Region 175. .400  
 FT /note= Human IgG1 Fc region lacking 1-5 residues  
 XX  
 WO200118203-A1.  
 PN 15-MAR-2001.  
 XX 18-AUG-2000; 2000WO-US022797.  
 XX 03-SEP-1999; 99US-00389782.  
 PR (AMGE-) AMGEN INC.  
 XX Dunstan CR, Wooden SK, Mann MB;  
 XX WPI; 2001-244572/25.  
 DR Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
 PT by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 XX  
 PS Claim 7; Fig 5; 119pp; English.  
 XX  
 CC The present sequence is a fusion protein comprising a sequence derived  
 CC from human osteoprotegerin (OPG; 22-194 residues) which is fused with  
 CC human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues by a  
 CC linker. OPG negatively regulates the formation of osteoclasts in vitro  
 CC and in vivo. It blocks the differentiation of osteoclasts from monocyte  
 CC or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion  
 CC protein is administered for the treatment of bone loss resulting from  
 CC osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia  
 CC associated with surgery or steroid administration, osteonecrosis, bone  
 CC loss due to rheumatoid arthritis, periodontal bone loss, osteolytic  
 CC metastasis and/or prosthetic loosening  
 XX  
 SQ Sequence 400 AA;

Query Match 96.8%; Score 2191; DB 4; Length 400;  
 Best Local Similarity 97.8%; Pred. No. 1.1e-128;  
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;  
 QY 1 ETTPPKYLHYDEBTSQQLCDKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETTPPKYLHYDEBTSQQLCDKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGFGVWVQAGTPERTV 120  
 DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIFCLKHSRCPGFGVWVQAGTPERTV 120  
 QY 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSGSESTOKSGGGGG 180  
 DB 121 CKRCPDGFFSNSTSSKAPCRKHTNCSVFGLLLTKGNATHDNCNSGSESTOKV----DK 176  
 QY 181 GGTCPCPAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 240  
 DB 177 THTCPCPAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGV 236  
 QY 241 EVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 300  
 DB 237 EVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 296  
 QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360  
 DB 297 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 356  
 QY 361 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404  
 DB 357 SPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 400

RESULT 10  
 AAB80902  
 ID AAB80902 standard; protein; 406 AA.  
 XX  
 AC AAB80902;  
 XX  
 DT 31-MAY-2001 (first entry)  
 XX  
 DE Human OPG(22-201)-FcDeltaC fusion protein.  
 XX  
 KW Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
 KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegerin;  
 KW osteoclast formation inhibition; bone resorption inhibition;  
 KW immunoglobulin.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200117543-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-US022806.  
 XX  
 PR 03-SRP-1999; 99US-00389545.  
 XX  
 PA (AMGB-) AMGEN INC.  
 XX  
 XX Dunstan CR;  
 XX  
 DR WPI; 2001-265936/27.  
 XX  
 XX Preventing or treating lytic bone diseases, particularly associated with  
 PT cancer or metastasis, by administering an osteoprotegerin polypeptide.  
 XX  
 PS Disclosure; Fig 6; 87pp; English.  
 XX  
 CC The present invention relates to a method for the prevention or treatment  
 CC of lytic bone disease or multiple myeloma. Also the method can be used  
 CC for preventing metastasis of cancer to bone or osteosclerotic bone  
 CC metastasis. The method comprises administering an OPG (osteoprotegerin)  
 CC polypeptide or OPG fusion protein. The present sequence is one such OPG  
 CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone  
 CC resorption) by blocking differentiation from monocytes/macrophage  
 CC precursors. The OPG polypeptide can be used in a method of preventing or  
 CC treating lytic bone disease, for preventing metastasis of cancer to bone  
 CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,  
 CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal  
 CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic  
 CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
 CC or treatment of loss of bone mass, which occurs in conditions including  
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC hyperthyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating

CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and  
 CC CH3 regions; see AAB80897-8)  
 XX  
 SQ Sequence 406 AA;

Query Match 96.8%; Score 2191; DB 4; Length 406;  
 Best Local Similarity 97.5%; Pred. No. 1.2e-128;  
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1 ETPPPKYLHYDEETSHQLLCKDKPPGTLYLKHCTAKWTVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETPPPKYLHYDEETSHQLLCKDKPPGTLYLKHCTAKWTVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVKQECNTHNRVCEKGRVLEIEFCLKHSRCPGFGVQAGTPTERTV 120  
 DB 61 YCSPVCKELQYVKQECNTHNRVCEKGRVLEIEFCLKHSRCPGFGVQAGTPTERTV 120  
 QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKSG- -GGG 178  
 DB 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKSGIDTV 180  
 QY 179 GGGTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 238  
 DB 181 DKHTCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 240  
 QY 239 GVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAK 298  
 DB 241 GVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAK 300  
 QY 299 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 358  
 DB 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 360  
 QY 359 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404  
 DB 361 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 406

RESULT 11

AA772920  
 ID AA772920 standard; protein; 406 AA.

AC AA772920;

DT 13-JUN-2001 (first entry)

DE Human OPG (22-201 aa)-Fc region (lacking 1-5 residues) fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 KW periodontal.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region

FT /note= "Derived from human osteoprotegerin fragment (22-  
 201 residues)"

FT Region

FT /label= Linker

FT Region

FT /note= Human IgG1 Fc region lacking 1-5 residues;

XX (Corresponds to 6-231 residues of IgG1 Fc region)

PN WO200118203-A1.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-US022797.

PF

XX 03-SEP-1999; 99US-00389782.  
 XX (AMGE-) AMGEN INC.  
 XX Dunstan CR, Wooden SK, Mann MB;  
 XX WPI; 2001-244572/25.  
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 XX Claim 7; Fig 6; 119pp; English.  
 XX The present sequence is a fusion protein comprising a sequence derived  
 XX from human osteoprotegerin (OPG; 22-201 residues) which is fused with  
 XX human immunoglobulin G1 (IgG1) Fc region lacking 1-5 residues, by a  
 XX linker. OPG negatively regulates the formation of osteoclasts in vitro  
 XX and in vivo. It blocks the differentiation of osteoclasts from monocyte  
 XX or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion  
 XX protein is administered for the treatment of bone loss resulting from  
 XX osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia  
 XX associated with surgery or steroid administration, osteonecrosis, bone  
 XX loss due to rheumatoid arthritis, periodontal bone loss, osteolytic  
 XX metastasis and/or prosthetic loosening  
 XX SQ Sequence 406 AA;  
 Query Match 96.8%; Score 2191; DB 4; Length 406;  
 Best Local Similarity 97.5%; Pred. No. 1.2e-128;  
 Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;  
 QY 1 ETPPKYLHYDEETSHQLLCKDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 DB 1 ETPPKYLHYDEETSHQLLCKDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120  
 DB 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120  
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSESSTQKSG--GGG 178  
 DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSESSTQKSGIDVTV 180  
 QY 179 GGGTCTPPCAPPELLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYD 238  
 DB 181 DKHTCTPPCAPPELLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYD 240  
 QY 239 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 298  
 DB 241 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300  
 QY 299 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 358  
 DB 301 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 360  
 QY 359 DGSFFLYSKLTVDKSRWQQGNVSCSWHEALHNNHYTKQSLSPG 404  
 DB 361 DGSFFLYSKLTVDKSRWQQGNVSCSWHEALHNNHYTKQSLSPG 406  
 RESULT 12  
 AAB66993  
 ID AAB66993 standard; protein; 422 AA.  
 XX AAB66993;  
 XX 19-APR-2001 (first entry)  
 XX OPG-Fc.  
 XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
 KW endometritis; fever; glomerulonephritis; inflammatory bowel disease;  
 KW ischaemia; Parkinson's disease.  
 XX Unidentified.  
 XX WO200103719-A2.  
 XX 18-JAN-2001.  
 XX 07-JUL-2000; 2000WO-US018667.  
 XX 09-JUL-1999; 99US-00350670.  
 XX 09-DEC-1999; 99US-00457647.  
 XX (AMGE-) AMGEN INC.  
 XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;  
 XX WPI; 2001-103031/11.  
 XX N-PSDB; AAF57869.  
 XX Treating conditions leading to bone loss such as rheumatoid arthritis,  
 XX multiple sclerosis and asthma, comprises administering an osteoprotegerin  
 XX protein in conjunction with e.g. inhibitors of interleukin and tumor  
 XX necrosis factor alpha.  
 XX Disclosure; Fig 29; 316pp; English.  
 XX The present invention relates to a method for treating conditions leading  
 XX to bone loss. The method comprises administering a purified and isolated  
 XX osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)  
 XX in conjunction with other substances such as tumour necrosis factor-alpha  
 XX (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
 XX modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet  
 XX activating factor (PAF) antagonists. The method is useful for treating  
 XX conditions leading to bone loss such as rheumatoid arthritis, multiple  
 XX sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
 XX useful for treating inflammation, systemic lupus erythematosus (SLE) and  
 XX graft-versus-host disease (GVHD). Other diseases that can be treated  
 XX include acute pancreatitis, Alzheimer's disease, anorexia,  
 XX atherosclerosis, coronary conditions (e.g. myocardial infarction),  
 XX cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
 XX inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
 XX psoriasis and septic shock  
 XX SQ Sequence 422 AA;  
 Query Match 96.8%; Score 2191; DB 4; Length 422;  
 Best Local Similarity 97.8%; Pred. No. 1.2e-128;  
 Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;  
 QY 1 ETPPKYLHYDEETSHQLLCKDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 60  
 DB 22 ETPPKYLHYDEETSHQLLCKDKCPGTYLKQHCTAKWTKVCAPCPDHYTDSWHTSDECL 81  
 QY 61 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 120  
 DB 82 YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGFGVVGAGTPERTV 141  
 QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSESSTQKSGGGG 180  
 DB 142 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCNSESSTQKV---DK 197  
 QY 181 GGTCTPPCAPPELLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYD 240  
 DB 198 THTCTPPCAPPELLGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYD 257  
 QY 241 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 300  
 DB 258 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 317

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QY 301 PREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 360
DB 318 PREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 377
QY 361 SFFLYSKLTVDKSRWQGNVFPSCVMHEALHNHYTQKSLSLSPG 404
DB 378 SFFLYSKLTVDKSRWQGNVFPSCVMHEALHNHYTQKSLSLSPG 421

RESULT 13
ABJ37103
ID ABJ37103 standard; protein; 659 AA.
XX
AC ABJ37103;
XX
DT 08-MAY-2003 (first entry)
XX
DE Concatameric immunoadhesion human protein sequence SEQ ID No 12.
XX
KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human.
XX
OS Homo sapiens.
XX
FN WO2003010202-A1.
XX
PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-KR001427.
XX
PR 26-JUL-2001; 2001KR-00045028.
XX
PA (MEDE-) MEDEXGEN CO LTD.
XX
PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
DR WPI; 2003-229639/22.
XX
DR N-PSDB; ABT32046.
XX
PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
PS Claim 27; Page 148-152; 21pp; English.
XX
CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammatory-
CC related diseases. This sequence represents the human concatameric protein
XX of the invention
XX
SQ Sequence 659 AA;

Query Match 66.3%; Score 1501.5; DB 6; Length 659;
Best Local Similarity 64.5%; Pred. No. 2.2e-85;
Matches 291; Conservative 18; Mismatches 81; Indels 61; Gaps 5;

QY 9 HYDEETSHQLCDKCPGPGTYLKHQCTAKWKTVCAPCPDHYHDTDSWHTSDCLYCSPVCKE 68
DB 214 YYDQ--TAQMCCSKSPGQGHAKVFCTKTSYDVCDSCESTYTLQNNWPECLSCGRSS 271
QY 69 LQVYQECNRTNVRVCECKEGRYLEI-----EFLKHSRCPGPGVQAGTPERTVCK 122
DB 272 DQVETQACTREQNRICTRPGWYCALSKQEGCRLCAPLKRCPGPGVARPGTETSDVYCK 331
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QY 123 RCPDGFSSNETSKAPCRKHTNCVFGLLLTOKGNATHDNCISGNSESTQKSGG----- 176
DB 332 PCARGTFSTNTSSTDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLBQ 387
QY 177 -----GGGGGG-----TCPPCPAPELL 193
DB 388 PVSTRSQHTQPTPEPSTAPSTFLLPMGPPSPAEGSTGDABPKSCDKHTHTCPPAPELL 447
QY 194 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRBEQ 253
DB 448 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRBEQ 507
QY 254 YNSTYRVVSVLTTLVHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 313
DB 508 YNSTYRVVSVLTTLVHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 567
QY 314 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 373
DB 568 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 627
QY 374 RWOQGNVFPSCVMHEALHNHYTQKSLSLSPG 404
DB 628 RWOQGNVFPSCVMHEALHNHYTQKSLSLSPG 659

RESULT 14
ADQ79910
ID ADQ79910 standard; protein; 659 AA.
XX
AC ADQ79910;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human tumour necrosis factor receptor 2, mgTNFR2-TNFR2/Ig construct.
XX
KW Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
KW immunoglobulin; concatameric fused dimer protein; immunoadhesin;
KW Fc fragment; hinge.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN KR2004009997-A.
XX
PD 31-JAN-2004.
XX
PF 26-JUL-2002; 2002KR-00045921.
XX
PR 26-JUL-2002; 2002KR-00045921.
XX
PA (MEDE-) MEDEXGEN INC.
XX
PI Choi EY, Han JU, Jung YH, Kim JM, Lee HJ;
XX
DR WPI; 2004-458871/43.
XX
DR N-PSDB; ADQ79909.
XX
PT Concatameric immunoadhesin.
XX
PS Claim 27; SEQ ID NO 12; 129pp; Korean.
XX
CC The invention relates to a concatameric fused dimer protein and
CC glycosylation modification protein providing concatameric immunoadhesin
CC with improved efficacy and stability. The concatameric protein is
CC characteristically formed by binding C-terminal of one biologically
CC active protein with N-terminal of same or different biologically active
CC protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
CC CTLA4. Two monomer proteins which are formed by fusing the extracellular
CC region of a protein participating in the same immune reaction to an
CC immunoglobulin Fc fragment, bound together at a hinge region by
CC disulphide bond to give the concatameric fused dimer protein, wherein the
CC immunoglobulin is IgG. The present sequence represents a monomeric or
```

[illegible]

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1481	65.4	518	1	US-08-385-229-4	Sequence 4, Appli
2	1481	65.4	518	4	US-09-579-845-1	Sequence 1, Appli
3	1481	65.4	518	4	US-09-579-845-3	Sequence 3, Appli
4	1477.5	65.3	486	1	US-08-243-010-1	Sequence 11, Appli
5	1332	58.8	360	3	US-09-180-100-11	Sequence 22, Appl
6	1332	58.8	376	3	US-09-180-100-22	Sequence 22, Appl
7	1324.5	58.5	398	4	US-09-613-033B-14	Sequence 14, Appl
8	1299	57.4	438	1	US-08-097-827-11	Sequence 11, Appl
9	1299	57.4	438	1	US-08-494-574-11	Sequence 11, Appl
10	1287.5	56.9	424	3	US-09-333-593A-8	Sequence 8, Appli
11	1245	55.0	397	4	US-09-854-864-18	Sequence 18, Appl
12	1242.5	54.9	283	4	US-09-854-864-9	Sequence 9, Appli
13	1242	54.9	281	4	US-09-854-864-10	Sequence 10, Appl
14	1236	54.6	257	4	US-09-428-082B-18	Sequence 18, Appl
15	1236	54.6	277	4	US-09-428-082B-20	Sequence 20, Appl
16	1233.5	54.5	269	4	US-09-428-082B-10	Sequence 10, Appl
17	1232	54.4	250	4	US-09-428-082B-1070	Sequence 1070, Ap
18	1231.5	54.4	911	2	US-08-484-438-10	Sequence 10, Appl
19	1228	54.2	704	4	US-09-590-656-2	Sequence 2, Appli
20	1228	54.2	704	4	US-09-733-764-2	Sequence 2, Appli
21	1223.5	54.0	455	4	US-09-773-877B-24	Sequence 24, Appl
22	1223.5	54.0	664	3	US-08-957-063-16	Sequence 16, Appl
23	1223.5	54.0	664	3	US-09-487-685-16	Sequence 16, Appl
24	1223.5	54.0	664	3	US-08-802-805D-16	Sequence 16, Appl
25	1223.5	54.0	664	4	US-09-388-161C-16	Sequence 16, Appl
26	1222.5	54.0	258	4	US-09-428-082B-1058	Sequence 1058, Ap
27	1222.5	54.0	242	4	US-09-428-082B-1066	Sequence 1066, Ap

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Db 74 YYDQ--TAQMCCKSCSPGQHAUFCTKTSYTDVCDSCEDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPTERTVCK 122
Db 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGPPAPAGSTGDEPKSCDKTHTCPPCPAPELLG 307
Qy 195 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
Qy 375 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517

RESULT 2
US-09-579-845-1
; Sequence 1, Application US/09579845
; Patent No. 6537540
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-1

Query Match 65.4%; Score 1481; DB 4; Length 518;
Best Local Similarity 63.6%; Pred. No. 3.1e-116;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

Qy 9 HYDEETSHQLLCKPPGTLYLKQHCCTAKWKTVCAPCPDHYVYDTSWHTSDECLYCSPVCKE 68
Db 74 YYDQ--TAQMCCKSCSPGQHAUFCTKTSYTDVCDSCEDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPTERTVCK 122
Db 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGPPAPAGSTGDEPKSCDKTHTCPPCPAPELLG 307
Qy 195 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487

US-09-579-845-1
; Sequence 1, Application US/09579845
; Patent No. 6537540
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-1

Query Match 65.4%; Score 1481; DB 4; Length 518;
Best Local Similarity 63.6%; Pred. No. 3.1e-116;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

Qy 9 HYDEETSHQLLCKPPGTLYLKQHCCTAKWKTVCAPCPDHYVYDTSWHTSDECLYCSPVCKE 68
Db 74 YYDQ--TAQMCCKSCSPGQHAUFCTKTSYTDVCDSCEDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPTERTVCK 122
Db 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGPPAPAGSTGDEPKSCDKTHTCPPCPAPELLG 307
Qy 195 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
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Qy 195 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
Qy 375 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCVMHEALHNHYTQKSLSLSPG 517

RESULT 3
US-09-579-845-3
; Sequence 3, Application US/09579845
; Patent No. 6537540
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-3

Query Match 65.4%; Score 1481; DB 4; Length 518;
Best Local Similarity 63.6%; Pred. No. 3.1e-116;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

Qy 9 HYDEETSHQLLCKPPGTLYLKQHCCTAKWKTVCAPCPDHYVYDTSWHTSDECLYCSPVCKE 68
Db 74 YYDQ--TAQMCCKSCSPGQHAUFCTKTSYTDVCDSCEDSTYTQIWNWVPECLSCGRCS 131
Qy 69 LQYVQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCTPPGFGVVOAGTPTERTVCK 122
Db 132 DQVETQACTREONRICTCRPGWYCALSKQEGCRLCAPLRCRPGFGVARGTETSDDVCK 191
Qy 123 RCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 177
Db 192 PCAPGTFSNTTSSDTCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPELLG 194
Db 248 PVSTRSHTQPTPEPSTAPSTSFLLPMGPPAPAGSTGDEPKSCDKTHTCPPCPAPELLG 307
Qy 195 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 314
Db 368 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 427
Qy 315 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 487
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QY 375 WOQGNVSCSVMHEALHNHYTKLSLSPG 404  
Db 488 WOQGNVSCSVMHEALHNHYTKLSLSPG 517

## RESULT 4

US-08-243-010-1  
; Sequence 1, Application US/08243010  
; Patent No. 5639597  
; GENERAL INFORMATION:  
; APPLICANT: Lauffer, Leander  
; APPLICANT: Zettlmeisel, Gerd  
; APPLICANT: Oquendo, Patricia  
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The  
; TITLE OF INVENTION: Production and Use Thereof  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/243,010  
; FILING DATE: 13-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/798,564  
; FILING DATE: 26-NOV-1991  
; APPLICATION NUMBER: DE P 40 37 837.3  
; FILING DATE: 28-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Einaudi, Carol P.  
; REGISTRATION NUMBER: 32,220  
; REFERENCE/DOCKET NUMBER: 02481-1132-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 486 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-243-010-1

Query Match 65.3%; Score 1477.5; DB 1; Length 486;  
Best Local Similarity 64.3%; Pred. No. 5.6e-116;  
Matches 288; Conservative 18; Mismatches 83; Indels 59; Gaps 5;  
QY 9 HYDEETSHOLLCDKCPGTYLKHCTAKWTVCAPCPDHVYTDSDWHTSDECLYCSVCKE 68  
Db 45 YDQ--TAQMCSCSPGGHAKVFCTYTDVCDSCSDSTYQLWVVECLSCGRCS 102  
QY 69 LQVVKQECNRTHNRVCEKGRYLEI-----EFLKHSRCPGFGVQAGTPERNTVCK 122  
Db 103 DQVETQACTREQNRICTRPGWYCALSKQGCRLCAPLKRPGFGVARGPTGTSVVC 162  
QY 123 RCPDGFNETSSKAPCRHTNCSVFLGLLLTQKGNATHDNI CSGNSESTQKSGG----- 176  
Db 163 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDVACTSTSTPTSMAPGAVHLFPQ 218  
QY 177 -----GGGGGCTCCPCPAPELLGGP 196  
Db 219 PVSTRSQHTOPTPEPTAPSTSTFLPMGSPPAEDPEPKSKDCKTHCTCCPCPAPELLGGP 278

QY 197 SVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 256  
Db 279 SVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 338  
QY 257 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSISKAKGQPREPQVYTLPPSRDEL 316  
Db 339 TYRVVSVLTVLHQ--WLNKGEYKCKVSNKALPAPIEKTSISKAKGQPREPQVYTLPPSRDEL 397  
QY 317 TKQVSLTCLVKGFPYSPDIAVWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 376  
Db 398 TKQVSLTCLVKGFPYSPDIAVWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 457  
QY 377 QGNVFSCSVMHEALHNHYTKLSLSPG 404  
Db 458 QGNVFSCSVMHEALHNHYTKLSLSPG 485  
RESULT 5  
US-09-180-100-11  
; Sequence 11, Application US/09180100  
; Patent No. 6306395  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: NAKAMURA, No. 6306395io  
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
; FILE REFERENCE: 1110-207P  
; CURRENT APPLICATION NUMBER: US/09/180,100  
; CURRENT FILING DATE: 1998-11-02  
; EARLIER APPLICATION NUMBER: PCT/JP97/01502  
; EARLIER FILING DATE: 1997-05-01  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-180-100-11  
Query Match 58.8%; Score 1332; DB 3; Length 360;  
Best Local Similarity 66.7%; Pred. No. 6.5e-104;  
Matches 270; Conservative 15; Mismatches 60; Indels 60; Gaps 11;  
QY 8 LHYDEETSHOLLCDKCPGTYLKHCTAKW-KTVCAPCPD-HYYTDSWHTSDECLYCSPV 65  
Db 7 LHHGQGFCHK-----PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCR-L 61  
QY 66 CKELQVVKQE--CNRTHNRVCEKGRYLEIEFLKHSRCP-----GFGVQAGTPERN 119  
Db 62 CDGEGHLEVEINCTRTQNTKCRKPNFNCNSTVC---EHCDFCTKCEHGIIECTLTSTNT 118  
QY 120 VCKRCPDGFNETSSKAPCRHTNCSVFLGLLLTQKGNATHDNI CSGNSESTQKSGGG 179  
Db 119 KCKE--EGSRNPEKS---CDK-----TH----- 137  
QY 180 GGGTCCPCPAPELLCGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 239  
Db 138 ---TCPPCPAPPELLCGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 194  
QY 240 VEVHNAKTKPREEQYNSYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSISKAG 299  
Db 195 VEVHNAKTKPREEQYNSYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSISKAG 254  
QY 300 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSD 359  
Db 255 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSD 314  
QY 360 GSFFLYSKLTVDKSRWQQGNVPCSMHEALHNHYTKLSLSPG 404  
Db 315 GSFFLYSKLTVDKSRWQQGNVPCSMHEALHNHYTKLSLSPG 359

## RESULT 6

US-09-180-100-22

```
; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAKAMURA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-180-100-22

Query Match      58.8%; Score 1332; DB 3; Length 376;
Best Local Similarity 66.7%; Pred. No. 6.9e-104;
Matches 270; Conservative 15; Mismatches 60; Indels 60; Gaps 11;

QY 8 LHYDETSQLLCDKCPGTYLKQHC-TAKW-KTVCA-CPD-HYYTDSWHTSDECLYCSPV 65
Db 23 LHHGDFCHK---PCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCR-L 77
QY 66 CKELQVVKQE--CNRTHNRVCECKEGRYLEIEFCLKHRS-CP- ---GFGVQAGTPERN 119
Db 78 CDHGGLVEINCTRTQNTQKCKNFFCNSTVC---EHCDCPTKCEHGIIECTLTST 134
QY 120 VKCRPDGPFNETSKAPCRKHTNCSVFGLLLTQKGNATHONI CSGNSESTQKSGGGG 179
Db 135 KCKE--EGSRNPEKS---CDK-----TH----- 153
QY 180 GGGTCCPCAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 239
Db 154 ---TCPCCAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 210
QY 240 VEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 299
Db 211 VEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 270
QY 300 QPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD 359
Db 271 QPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD 330
QY 360 GSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Db 331 GSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 375

RESULT 7
US-09-612-033B-14
; Sequence 14, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

Query Match      58.5%; Score 1324.5; DB 4; Length 398;
Best Local Similarity 65.7%; Pred. No. 3.2e-103;
Matches 259; Conservative 24; Mismatches 62; Indels 49; Gaps 6;

QY 12 EETSHQLLCDKCPGTYLKQHC-TAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKELQ 70
Db 52 EYMSKDVCCCKNCAGTFVKAPCEIPHTQGCQCKCHPGTFTKDNLYDACILCS-TCRDKQ 110
QY 71 YVQECNRTNHRVCECKEGRYLEIEFCLKHRS-CPGFGVQAGTPERNVTCRCRCPDGFFS 130
Db 111 EWADCSATSDRKQCRTGLY-----YDPKF-----PESCRPTCKCQ----- 149
QY 131 NETSKAPCRKHTNCSVFGLLLTQKGNATHONI CSGNSESTQKSGGGGGTCCPPCAP 190
Db 150 -----GIPVQECNSTANTVCSSSVSNVDTH-----TCPPCAP 183
QY 191 ELLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 250
Db 184 ELLGGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 243
QY 251 BEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 310
Db 244 BEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 303
QY 311 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 370
Db 304 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 363
QY 371 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Db 364 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG 397

RESULT 8
US-09-612-033B-11
; Sequence 11, Application US/08097827
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: Novel Cytokine which is a Ligand for
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-Jul-1993
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
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```
;
;
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-097-827-11

Query Match          57.4%; Score 1299; DB 1; Length 438;
Best Local Similarity 60.4%; Pred. No. 5e-101;
Matches 258; Conservative 22; Mismatches 77; Indels 70; Gaps 6;

QY 20 CDKCPPTGYLKQHTAKWTKVCAPCPDHYTD--SWHTSDECLYCSVCKELQYVKQECN 77
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 39 CRECPQGHGMVNRCDHTRDTLCHPCETGTFYNEAVNYDTCKQCTQCNH--RSGSELQNCT 96
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 78 RTHNRVCECKEGYLEIEFCLKHRSCPPGFGVVQAGTPERNVTCKRCPDGFFSNETSSKA 137
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 97 PTQDTVCRCR-----PGTQPRQDSGYKLGVDVCPGPHFS--PGNNQ 137
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNICGNS----- 168
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 138 ACKPWTNCTLSGKQTRHPASDSLDVACEDRSLLATLLMETQRTPTTQSTVWPRTS 197
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 169 -----ESTQKSGGGGGGTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEV 217
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 198 ELPSTPTLVEPRSCDKT-----HTCPCPAPAEAGAPSVFLFPPKPKDTLMISRTPEV 250
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 218 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVVLTVLHODWLNKEY 277
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 251 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVVLTVLHODWLNKEY 310
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 278 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 311 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 370
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 338 EWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTOK 397
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 371 EWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTOK 430
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 398 SLSLSPG 404
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 431 SLSLSPG 437

RESULT 9
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783665el Cytokine which is a Ligand for
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR FILING DATE: 1997-05-09
```

```
;
;
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match          57.4%; Score 1299; DB 1; Length 438;
Best Local Similarity 60.4%; Pred. No. 5e-101;
Matches 258; Conservative 22; Mismatches 77; Indels 70; Gaps 6;

QY 20 CDKCPPTGYLKQHTAKWTKVCAPCPDHYTD--SWHTSDECLYCSVCKELQYVKQECN 77
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 39 CRECPQGHGMVNRCDHTRDTLCHPCETGTFYNEAVNYDTCKQCTQCNH--RSGSELQNCT 96
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 78 RTHNRVCECKEGYLEIEFCLKHRSCPPGFGVVQAGTPERNVTCKRCPDGFFSNETSSKA 137
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 97 PTQDTVCRCR-----PGTQPRQDSGYKLGVDVCPGPHFS--PGNNQ 137
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 138 PCRKHTNCSVFGLLLTQKGNATHDNICGNS----- 168
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 138 ACKPWTNCTLSGKQTRHPASDSLDVACEDRSLLATLLMETQRTPTTQSTVWPRTS 197
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 169 -----ESTQKSGGGGGGTCPPCPAPELLGSPVFLFPPKPKDTLMISRTPEV 217
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 198 ELPSTPTLVEPRSCDKT-----HTCPCPAPAEAGAPSVFLFPPKPKDTLMISRTPEV 250
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 218 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVVLTVLHODWLNKEY 277
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 251 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVVLTVLHODWLNKEY 310
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 278 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 311 KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 370
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 338 EWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTOK 397
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 371 EWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTOK 430
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 398 SLSLSPG 404
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 431 SLSLSPG 437

RESULT 10
US-09-333-593A-8
; Sequence 8, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R. A.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; TITLE OF INVENTION: TR6
; FILE REFERENCE: GH-50008-2
; CURRENT APPLICATION NUMBER: US/09/333,593A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
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Db 199 VSLTCLVKGFPSPDIAVEWESNGQPNYYKTPPVLDSDGSPFLYSLKLTVDKSRWQGNV 258
Qy 381 FSCVMHEALHNYTKSLSPG 404
Db 259 FSCVMHEALHNYTKSLSPG 282
RESULT 13
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
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Best Local Similarity 84.7%; Pred. No. 1.7e-96;
Matches 238; Conservative 5; Mismatches 24; Indels 14; Gaps 3;
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Db 10 YFDSLHACKPC---HURCS-----NPPATCQPYCDPSVTSVSGVYTGSGGGGDKTHT 59
Qy 184 CPDPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 243
Db 60 CPDPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 119
Qy 244 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 303
Db 120 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 179
Qy 304 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 363
Db 180 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 239
Qy 364 LYSKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 404
Db 240 LYSKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 280
RESULT 14
US-09-428-082B-18
; Sequence 18, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; CURRENT APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-FC
US-09-428-082B-18
Query Match 54.6%; Score 1236; DB 4; Length 253;
Best Local Similarity 97.5%; Pred. No. 4.8e-96;
Matches 230; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
Qy 173 KSGGGGGGG---TCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 228
Db 41 KPQGGGGGGDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 100
Qy 229 PEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 288
Db 101 PEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 160
Qy 289 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 348
Db 161 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 220
Qy 349 YKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 404
Db 221 YKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 276
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; SEQ ID NO 18
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: EMP-FC
US-09-428-082B-18
Query Match 54.6%; Score 1236; DB 4; Length 253;
Best Local Similarity 97.5%; Pred. No. 4.8e-96;
Matches 230; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
Qy 173 KSGGGGGGG---TCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 228
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Qy 229 PEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 288
Db 77 PEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 136
Qy 289 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 348
Db 137 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 196
Qy 349 YKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 404
Db 197 YKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 252
RESULT 15
US-09-428-082B-20
; Sequence 20, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-EMP-FC
US-09-428-082B-20
Query Match 54.6%; Score 1236; DB 4; Length 277;
Best Local Similarity 97.5%; Pred. No. 5.4e-96;
Matches 230; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
Qy 173 KSGGGGGGG---TCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 228
Db 41 KPQGGGGGGDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 100
Qy 229 PEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 288
Db 101 PEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 160
Qy 289 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 348
Db 161 PIEKTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 220
Qy 349 YKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 404
Db 221 YKTPPVLDSDGSPFLYSLKLTVDKSRWQGNVFSVCSVMHEALHNYTKSLSPG 276
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 61.0417 Seconds  
(without alignments)  
2177.757 Million cell updates/sec

Title: US-09-389-782A-7  
Perfect score: 2264  
Sequence: 1 ETFFPKYLHYDETSQLLC.....VMHEALNNHYTQKSLSPG 404

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Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2264	100.0	404	10	US-09-389-782-7
2	2199	97.1	425	16	US-10-467-243-20
3	2192.5	96.8	413	10	US-09-389-782-4
4	2191.5	96.8	407	10	US-09-389-782-3
5	2191	96.8	400	10	US-09-389-782-5
6	2191	96.8	406	10	US-09-389-782-6
7	1501.5	66.3	659	14	US-10-363-427-12
8	1496	66.1	467	17	US-10-901-735-4
9	1493.5	66.0	490	14	US-10-363-427-4
10	1493.5	66.0	720	14	US-10-363-427-8
11	1481	65.4	518	14	US-10-313-852-1
12	1481	65.4	518	14	US-10-313-852-3
13	1481	65.4	518	14	US-10-314-033-1
					Sequence 7, Appli
					Sequence 20, Appli
					Sequence 4, Appli
					Sequence 3, Appli
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 12, Appli
					Sequence 4, Appli
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 1, Appli

14	1481	65.4	518	14	US-10-314-033-3	Sequence 3, Appli
15	1481	65.4	518	15	US-10-423-507-1	Sequence 1, Appli
16	1436.5	63.4	444	16	US-10-467-243-24	Sequence 24, Appli
17	1435.5	63.4	443	14	US-10-151-071-5	Sequence 5, Appli
18	1435.5	63.4	443	14	US-10-166-232A-5	Sequence 5, Appli
19	1361.5	60.1	608	14	US-10-363-427-10	Sequence 10, Appli
20	1353.5	59.8	444	14	US-10-363-427-2	Sequence 2, Appli
21	1353.5	59.8	628	14	US-10-363-427-6	Sequence 6, Appli
22	1332	58.8	360	9	US-09-949-713-11	Sequence 11, Appli
23	1332	58.8	376	9	US-09-949-713-22	Sequence 22, Appli
24	1332	58.8	376	14	US-10-084-139-10	Sequence 10, Appli
25	1325.5	58.5	396	14	US-10-193-616-14	Sequence 14, Appli
26	1324.5	58.5	398	15	US-10-622-407-14	Sequence 14, Appli
27	1257.5	55.5	347	15	US-10-272-899A-108	Sequence 108, Appli
28	1252.5	55.3	380	9	US-09-948-018-39	Sequence 39, Appli
29	1246	55.0	404	9	US-09-948-018-16	Sequence 16, Appli
30	1245	55.0	397	9	US-09-854-864-18	Sequence 18, Appli
31	1245	55.0	397	9	US-09-855-158-18	Sequence 18, Appli
32	1243	54.9	446	9	US-09-792-200B-10	Sequence 10, Appli
33	1242.5	54.9	283	9	US-09-854-864-9	Sequence 9, Appli
34	1242.5	54.9	283	9	US-09-855-158-9	Sequence 9, Appli
35	1242	54.9	281	9	US-09-854-864-10	Sequence 10, Appli
36	1242	54.9	281	9	US-09-855-158-10	Sequence 10, Appli
37	1240	54.8	462	15	US-10-385-802-32	Sequence 32, Appli
38	1240	54.8	489	15	US-10-385-802-30	Sequence 30, Appli
39	1240	54.8	588	15	US-10-385-802-28	Sequence 28, Appli
40	1240	54.8	648	15	US-10-385-802-24	Sequence 24, Appli
41	1240	54.8	665	15	US-10-385-802-26	Sequence 26, Appli
42	1240	54.8	697	15	US-10-385-802-48	Sequence 48, Appli
43	1240	54.8	705	15	US-10-385-802-22	Sequence 22, Appli
44	1240	54.8	726	15	US-10-385-802-20	Sequence 20, Appli
45	1240	54.8	883	15	US-10-385-802-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-389-782-7  
; Sequence 7, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-7

Query Match 100.0%; Score 2264; DB 10; Length 404;  
Best Local Similarity 100.0%; Pred. No. 9,7e-137;  
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	ETFFPKYLHYDETSQLLC	CDKCPGTYLKQHKTA	KWKVCAPCPDHYTDS	SHHTSDECL 60
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Db	61	YCSPVCKELQYVKQECNR	THNRVCECKGRYLEIF	ECLKHRS	CPGFGVVGACGP
QY	121	CKRCPDGFPSNETSSKAP	CKRHTNC	SVFGLLLTQKGNATHD	NCISGNSBSTQSGGGGG 180
Db	121	CKRCPDGFPSNETSSKAP	CKRHTNC	SVFGLLLTQKGNATHD	NCISGNSBSTQSGGGGG 180

QY 181 GGTCCPPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240  
DB 181 GGTCCPPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240  
QY 241 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQ 300  
DB 241 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQ 300  
QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDG 360  
DB 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDG 360  
QY 361 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPG 404  
DB 361 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPG 404

## RESULT 2

US-10-467-243-20  
; Sequence 20, Application US/10467243  
; Publication No. US20040132971A1  
; GENERAL INFORMATION:  
; APPLICANT: Maxygen Holdings Ltd.  
; APPLICANT: Haaning, Jesper Mortensen  
; APPLICANT: Haikier, Torben  
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES  
; FILE REFERENCE: 0226wo310  
; CURRENT APPLICATION NUMBER: US/10/467,243  
; PRIOR FILING DATE: 2003-08-06  
; PRIOR APPLICATION NUMBER: DK PA 2001 00214  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/267,843  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: DK PA 2001 00498  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 60/278,320  
; PRIOR FILING DATE: 2001-03-23  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: OPG-Fc polypeptide encoded by SEQ ID NO:19  
US-10-467-243-20

Query Match 97.1%; Score 2199; DB 16; Length 425;  
Best Local Similarity 97.8%; Pred. No. 1.4e-132;  
Matches 395; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTOKSGGGG 180  
DB 142 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTOKLEKSDK 201  
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DB 202 THTCPPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 261  
QY 241 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQ 300  
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QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDG 360

DB 322 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDG 381  
QY 361 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPG 404  
DB 382 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPG 425

## RESULT 3

US-09-389-782-4  
; Sequence 4, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-4

Query Match 96.8%; Score 2192.5; DB 10; Length 413;  
Best Local Similarity 95.9%; Pred. No. 3.7e-132;  
Matches 396; Conservative 0; Mismatches 8; Indels 9; Gaps 1;  
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QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTOKSGGGG 180  
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QY 232 KFNWYVDGVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 291  
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QY 292 KTISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKT 351  
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DB 361 TPPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPG 413

## RESULT 4

US-09-389-782-3  
; Sequence 3, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-3

Query Match
Best Local Similarity 96.8%; Score 2191.5; DB 10; Length 407;
Matches 395; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEIFCLKHSRCPGFGVVGAGTPTERTV 120
DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEIFCLKHSRCPGFGVVGAGTPTERTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSBSTQSGG--G 177
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSBSTQSGG--G 177
QY 178 GGGGTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 237
DB 178 GGGGTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 237
QY 181 CDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 240
DB 181 CDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 240
QY 238 DGVEVHNATKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYCKKVSNNKALPAPIEKTISKA 297
DB 241 DGVEVHNATKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYCKKVSNNKALPAPIEKTISKA 300
QY 298 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 357
DB 301 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
QY 358 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 404
DB 361 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 407

RESULT 5
US-09-389-782-5
; Sequence 5, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-5

Query Match
Best Local Similarity 96.8%; Score 2191; DB 10; Length 400;
Matches 395; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEIFCLKHSRCPGFGVVGAGTPTERTV 120
DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEIFCLKHSRCPGFGVVGAGTPTERTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSBSTQSGG--G 178
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSBSTQSGG--G 178
QY 179 GGGGTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 238
DB 181 DKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 240
QY 239 GVEVHNATKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYCKKVSNNKALPAPIEKTISKA 298
DB 241 GVEVHNATKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYCKKVSNNKALPAPIEKTISKA 300
QY 299 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 358
DB 301 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
QY 359 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 404
DB 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 406

RESULT 6
US-09-389-782-6
; Sequence 6, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-6

Query Match
Best Local Similarity 96.8%; Score 2191; DB 10; Length 406;
Matches 396; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEIFCLKHSRCPGFGVVGAGTPTERTV 120
DB 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLIEIFCLKHSRCPGFGVVGAGTPTERTV 120
QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSBSTQSG--GGG 178
DB 121 CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSBSTQSG--GGG 178
QY 179 GGGGTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 238
DB 181 DKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 240
QY 239 GVEVHNATKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYCKKVSNNKALPAPIEKTISKA 298
DB 241 GVEVHNATKPREEQYNSTYRVSVLTVLHQDLNGLNGKEYCKKVSNNKALPAPIEKTISKA 300
QY 299 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 358
DB 301 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 360
QY 359 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 404
DB 361 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 406
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RESULT 7
US-10-363-427-12
; Sequence 12, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: MeDexGen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Woong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatametric Immunoadhesion
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 12
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-427-12

Query Match 66.3%; Score 1501.5; DB 14; Length 659;
Best Local Similarity 64.5%; Pred No. 8.1e-88;
Matches 291; Conservative 18; Mismatches 81; Indels 61; Gaps 5;

Qy 9 HYDETSQHLCDCKPPGTYLKOHCTAKWTVCAPCPDHYDTSWHTSDCLYCSPVCKE 68
Db 214 YDQ--TAQMCCSCSPQHAQVCTKTSDTVDCSDSTVTQLWNWVPECLSCGRCS 271
Qy 69 LOYVKQCNTRHNVCKCKGRYLEI-----BFLKXHRCPPGFGVGVQAGTPERNVCK 122
Db 272 DQVETQACTREQNRICTRCPGWYCALSKQBGCRLCAPLRCRPGFGVARPGTETSDVVK 331
Qy 123 RCPDGFESNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 176
Db 332 PCAPGTFSNTSSDICKRPHQICNVAI----PGNASMDAVCTSTSTSRSMAPGAVHLPO 387
Qy 177 -----GGGGGG-----TCPCCPAPELL 193
Db 388 PVSTRSHTQTPETPSTAPSTSLFLPMGPPPAEGSTGDAEPKSCDXHTTCCPCPAPELL 447
Qy 194 GGFSVLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 253
Db 448 GGFSVLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 507
Qy 254 YNSTYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 313
Db 508 YNSTYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 567
Qy 314 DELTKNQVSLTCLVKGYFSPYDIAVEHESGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 373
Db 568 DELTKNQVSLTCLVKGYFSPYDIAVEHESGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 627
Qy 374 RWQQGNVFCSVNMHEALHNHYTQKSLSLSPG 404
Db 628 RWQQGNVFCSVNMHEALHNHYTQKSLSLSPG 658

RESULT 8
US-10-901-735-4
; Sequence 4, Application US/10901735
; Publication No. US20050032183A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN, Inc.
; APPLICANT: OSSLUND, Timothy D.
; APPLICANT: CLOGSTON, Christi
; APPLICANT: CRAMPTON, Shon
; APPLICANT: BASS, Randal
; TITLE OF INVENTION: CRYSTALLINE POLYPEPTIDES
; FILE REFERENCE: A-859

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Qy	123	RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNTCSGNSSESTQKSGG-----	170
Db	393	PCAPGTFTSNTSSDTCRPHQICNVVAI-----PGNASMDAVACTSTSPTRSMAPGAVHLDPQ	448
Qy	177	-----GGGGGG-----TCPPCPAPELL	193
Db	449	PVSTRSHTQTPPEPSTAPSTSFLPMGPPSPAGSGTGDAEPKSCDKTHTCTCPPCPAPELL	508
Qy	194	GGPSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREEQ	253
Db	509	GGPSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREEQ	568
Qy	254	YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAQGPQREPOVYTLPPSR	313
Db	569	YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAQGPQREPOVYTLPPSR	628
Qy	314	DELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS	373
Db	629	DELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS	688
Qy	374	RWQOGNVFSCVMHEALHNHYTQKSLSLSPG	404
Db	689	RWQOGNVFSCVMHEALHNHYTQKSLSLSPG	719
RESULT 11			
US-10-313-852-1			
; Sequence 1, Application US/10313852			
; Publication No. US20030103942A1			
; GENERAL INFORMATION:			
; APPLICANT: Burstein, Haim			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING			
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCI			
; TITLE OF INVENTION: DISORDERS			
; FILE REFERENCE: 226272004420			
; CURRENT APPLICATION NUMBER: US/10/313,852			
; CURRENT FILING DATE: 2002-12-06			
; PRIOR APPLICATION NUMBER: US/09/579,845			
; PRIOR FILING DATE: 2000-05-26			
; PRIOR APPLICATION NUMBER: 60/150,688			
; PRIOR FILING DATE: 1999-05-28			
; NUMBER OF SEQ ID NOS: 20			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 518			
; TYPE: PRT			
; ORGANISM: Homo sapien			
US-10-313-852-1			
Query Match 65.4%; Score 1481; DB 14; Length 518;			
Best Local Similarity 63.6%; Pred. No. 1.3e-86;			
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5			
Qy	9	HYDEETSHQLLCDKCPPTGYTLKCRCTAKWKTVCAPCPDPHYTDSWHTSDCLYCSFVCKE	68
Db	74	YDQ--TAQMCCSKCSGQHAQVCTKTSIDVDCSDSTVTLNWNWPECLSCGSRCS	131
Qy	69	LQYVKQECNRTHNVCECKEGRYLEI-----EFLCHKRSCPPPGVGVQAGTPERTVCK	122
Db	132	DQVETQACTREONRICTCRPGWCALSKQEGCRLCAPLRKCRPGFVARPGTETSDVVCK	191
Qy	123	RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNTCSGNSSESTQKSGG-----	177
Db	192	PCAPGTFTSNTSSDTCRPHQICNVVAI-----PGNASMDAVACTSTSPTRSMAPGAVHLDPQ	247
Qy	178	-----GGGGGG-----TCPPCPAPELL	194
Db	248	PVSTRSHTQTPPEPSTAPSTSFLPMGPPSPAGSGTGDEPKSCDKTHTCTCPPCPAPELL	307
Qy	195	GPSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREEQ	254
Db	308	GPSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREEQ	367

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Qy 255 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 314
Db 368 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
Qy 315 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487
Qy 375 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 517

RESULT 12
US-10-313-852-3
; Sequence 3, Application US/10313852
; Publication No. US20030103942A1
; GENERAL INFORMATION:
; APPLICANT: Burstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/10/313,852
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/579,845
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-313-852-3

Query Match 65.4%; Score 1481; DB 14; Length 518;
Best Local Similarity 63.6%; Pred. No. 1.3e-86;
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;

Qy 9 HYDEETSHQLLCKDKCPGTVLKQHCTAKWTVACAPCPDHVYTDSDCLYCSPVCKE 68
Db 74 YYDQ--TAQCCSKCSPGQAHKVFCTYSTVDCSDCEDSTYTQLMNWVPECLSCGRCS 131
Qy 69 LQVKGECNTHNRVCEKEGRYLEI-----BFCLKHRSCPPGFGVQAGTPERNTVK 122
Db 132 DQVETOACTREQNKRICTCRPGWCALSKQGBRCCLCAPLRCRPGFVGARGTETSDVCK 191
Qy 123 RCPDGFESNETSKAPCRKHTNCSVGLLLTQGNATHNICSGNESESTQKSGG----- 177
Db 192 PCAPGTFSTNTSDTDCRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHL 247
Qy 178 -----GGGG-----TCPPCPAPPELLG 194
Db 248 PVSTRSQHTQPTPEPSTAPSTSFLLPMGRSPPAEGSTGDEPKSCDKTHCTPPCPAPELLG 307
Qy 195 GPSVFLLPFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 254
Db 308 GPSVFLLPFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 367
Qy 255 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 314
Db 368 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 427
Qy 315 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 374
Db 428 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487
Qy 375 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 404
Db 488 WOQGNVFSCSVMHEALHNHYTQKSLSLSPG 517

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TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED  
DISORDERS  
FILE REFERENCE: 226272004420  
CURRENT APPLICATION NUMBER: US/10/314,033  
PRIORITY FILING DATE: 2002-12-06  
PRIORITY FILING DATE: 2002-12-06  
PRIORITY FILING DATE: 2000-05-26  
PRIORITY FILING DATE: 2000-05-26  
PRIORITY FILING DATE: 1999-05-28  
PRIORITY FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 518  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-314-033-3

Query Match 65.4%; Score 1481; DB 14; Length 518;  
Best Local Similarity 63.6%; Pred. No. 1.3e-86;  
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;  
QY 9 HYDEETSHQLCDKCPPEGYLKHQCTAKWKTVCAPCPDHYHDTSWHTSDCLYCSPVCKE 68  
DB 74 YDQ--TAQWCCSKCSPGQAHKVFCTKTSVTCDSCDSTYTLQMNWVPECLSCGSRCS 131  
QY 69 LQVVKQECNTHNRVCEKGRYLEI-----EFCLKHRSCTPPGFGVVGAGTPERNTVCK 122  
DB 132 DQVETQACTREQNRICTRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVK 191  
QY 123 RCPDGFESNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 177  
DB 192 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247  
QY 178 -----GGGG-----TCPPCPAPPELLG 194  
DB 248 PVSTRSQHTQPTPEPTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCPPCPAPELLG 307  
QY 195 GPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 254  
DB 308 GPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 367  
QY 255 NSTYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 314  
DB 368 NSTYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 427  
QY 315 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 374  
DB 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487  
QY 375 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 404  
DB 488 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 517

RESULT 15  
US-10-423-507-1  
Sequence 1, Application US/10423507  
Publication No. US20030219735A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Barrie, J.  
TITLE OF INVENTION: METABOLICALLY ACTIVATED RECOMBINANT  
VIRAL VECTORS AND METHODS FOR THEIR PREPARATION AND USE  
FILE REFERENCE: 226272004302  
CURRENT APPLICATION NUMBER: US/10/423,507  
PRIORITY FILING DATE: 2003-04-25  
PRIORITY FILING DATE: 2000-08-08  
PRIORITY FILING DATE: 2000-08-08  
PRIORITY FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 518

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-423-507-1  
Query Match 65.4%; Score 1481; DB 15; Length 518;  
Best Local Similarity 63.6%; Pred. No. 1.3e-86;  
Matches 286; Conservative 21; Mismatches 83; Indels 60; Gaps 5;  
QY 9 HYDEETSHQLCDKCPPEGYLKHQCTAKWKTVCAPCPDHYHDTSWHTSDCLYCSPVCKE 68  
DB 74 YDQ--TAQWCCSKCSPGQAHKVFCTKTSVTCDSCDSTYTLQMNWVPECLSCGSRCS 131  
QY 69 LQVVKQECNTHNRVCEKGRYLEI-----EFCLKHRSCTPPGFGVVGAGTPERNTVCK 122  
DB 132 DQVETQACTREQNRICTRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVK 191  
QY 123 RCPDGFESNETSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGG----- 177  
DB 192 PCAPGTFSNTTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPQ 247  
QY 178 -----GGGG-----TCPPCPAPPELLG 194  
DB 248 PVSTRSQHTQPTPEPTAPSTSFLLPMGPSPPAEGSTGDEPKSCDKTHTCPPCPAPELLG 307  
QY 195 GPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 254  
DB 308 GPSVFLFPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 367  
QY 255 NSTYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 314  
DB 368 NSTYRVSVSLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 427  
QY 315 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 374  
DB 428 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSR 487  
QY 375 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 404  
DB 488 WOQGNVFSCSVMEALHNHYTQKSLSLSPG 517

Search completed: March 8, 2005, 15:16:16  
Job time : 69.0417 sec

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.4652 Seconds  
(without alignments)  
2360.831 Million cell updates/sec

Title: US-09-389-782a-7  
Perfect score: 2264  
Sequence: 1 EYFPKYLHYDETSHQLLC.....VMHEALHNHYTKSLSLSPG 404

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1204	53.2	255	4 S31866	Ig gamma-1 chain C
2	1204	53.2	330	1 GHU	Ig gamma-1 chain C
3	1198	52.9	374	2 S69339	Ig heavy chain V r
4	1162	51.3	234	2 PT0207	Ig gamma chain C r
5	1146.5	50.6	377	2 A23511	Ig gamma-3 chain C
6	1144.5	50.6	377	2 A60764	Ig gamma-3 chain C
7	1137.5	50.2	326	1 G2HU	Ig gamma-2 chain C
8	1133	50.0	327	1 G4HU	Ig gamma-4 chain C
9	1125.5	49.7	289	1 G3HUI	Ig gamma-3 heavy C
10	909	40.2	323	1 GHRB	Ig gamma chain C r
11	902.5	39.9	328	2 I47160	Ig gamma 2b chain
12	902.5	39.9	328	2 I47159	Ig gamma 2a chain
13	900.5	39.8	277	2 I47162	Ig gamma 4 chain C
14	890.5	39.3	329	1 G2GP	Ig gamma-2 chain C
15	880.5	38.9	328	2 I47158	Ig gamma 1 chain c
16	874.5	38.6	328	2 I47161	Ig gamma 3 chain c
17	850.5	37.6	470	2 S22080	Ig heavy chain pre
18	841.5	37.2	329	1 G3MSC	Ig gamma-3 chain C
19	841	37.1	308	2 C30554	Ig heavy chain C r
20	841	37.1	472	2 S31459	Ig gamma-1 chain -
21	840	37.1	333	2 PS0018	Ig gamma-2b chain
22	835.5	36.9	398	1 G3MSM	Ig gamma-3 chain C
23	824.5	36.4	326	2 PS0017	Ig gamma-1 chain C
24	822.5	36.3	444	2 PC4436	monoclonal antibod
25	812.5	35.9	334	1 G1MS	Ig gamma-1 chain C
26	812.5	35.9	331	1 G1MSM	Ig gamma-1 chain C
27	804.5	35.5	329	2 S00847	Ig gamma-2c chain
28	804	35.5	330	1 G2MSA	Ig gamma-2a chain
29	804	35.5	399	1 G2MSAM	Ig gamma-2a chain

30	804	35.5	469	2 S37483	Ig gamma-2a chain
31	797	35.2	335	1 G2MSAB	Ig gamma-2a chain
32	794	35.1	446	2 S40295	Ig gamma-2a chain
33	780.5	34.5	322	2 PS0019	Ig gamma-2a chain
34	774	34.2	405	1 G2MSBM	Ig gamma-2b chain
35	774	34.2	474	1 G2MS11	Ig gamma-2b chain
36	760.5	33.6	327	2 S06611	Ig gamma-2 chain C
37	752	33.2	475	2 S01321	Ig gamma-2b chain
38	702	31.0	180	2 I46732	Ig gamma heavy cha
39	577.5	25.5	249	2 S69340	Ig heavy chain VHI
40	574.5	25.4	218	2 A36040	Ig heavy chain V-I
41	566	25.0	152	2 S14236	Ig gamma-1 chain C
42	402	17.8	572	2 B46529	Ig Y heavy chain (
43	361	15.9	549	2 S04845	Ig heavy chain pre
44	360.5	15.9	391	1 MHUHT	Ig mu heavy chain
45	357.5	15.8	343	2 S25644	Ig mu chain C regi

ALIGNMENTS

RESULT 1

S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R:Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products.  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 53.2%; Score 1204; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 2e-67; Indels 0; Gaps 0;  
Matches 222; Conservative 0; Mismatches 0;

QY	183	TCPPCPAPELLGGPSVFLPPPKD	TLMSRTEVTCVVVDVSHEDPEVKFNMYVDGVEV	242
DB	33	TCPPCPAPELLGGPSVFLPPPKD	TLMSRTEVTCVVVDVSHEDPEVKFNMYVDGVEV	92
QY	243	HNAKTKPREEQNSTYRVVSVLT	VLHODWLNKCKYKCKVSNKALPAPIETISKAKGQPR	302
DB	93	HNAKTKPREEQNSTYRVVSVLT	VLHODWLNKCKYKCKVSNKALPAPIETISKAKGQPR	152
QY	303	BPQVTLTPSRDELTKNOVSLT	CLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSF	362
DB	153	BPQVTLTPSRDELTKNOVSLT	CLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSF	212
QY	363	FLYSKLTVDKSRWQQGNVFPSC	SMHEALHNHYTKSLSLSPG	404
DB	213	FLYSKLTVDKSRWQQGNVFPSC	SMHEALHNHYTKSLSLSPG	254

RESULT 2

GHU  
Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA

A;Residues: 1-330 <ELL>  
A;Cross-references: UNIPROT:P01857; EMBL:Z17370  
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,  
R;Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S33904  
A;Accession: S36861  
A;Molecule type: DNA  
A;Residues: 2-330 <HAR>  
A;Cross-references: EMBL:Z17370  
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A;Reference number: S33887; MUID:83001943; PMID:6811139  
A;Accession: S33887  
A;Molecule type: DNA  
A;Residues: 88-113;235-330 <TAK>  
A;Cross-references: EMBL:Z17370  
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
Biochemistry 9, 3161-3170, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A;Reference number: A90563; MUID:71064024; PMID:5489771  
A;Contents: myeloma protein Eu  
A;Accession: B90563  
A;Molecule type: protein  
A;Residues: 1-96,'R',98-135 <CUN>  
A;Note: this sequence has the G1m(3) marker, 97-Arg  
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A;Reference number: A90564; MUID:71064025; PMID:5530842  
A;Contents: Eu  
A;Accession: A90564  
A;Molecule type: protein  
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,  
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R;Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668  
A;Molecule type: protein  
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
A;Note: this sequence has the G1m(17) and G1m(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO1  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KO1; disulfide bonds  
A;Accession: A91723  
A;Molecule type: protein  
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH  
A;Note: this sequence has the G1m(3) and G1m(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enamide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1002129  
A;Contents: annotation; disulfide bonds  
A;Genetics:  
A;Gene: GDB:IGHG1  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1, 114/1, 224/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;137-206/Domain: immunoglobulin homology <IM2>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83,144-204,250-308/Disulfide bonds: #status experimental  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 53.2%; Score 1204; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 2.6e-67;  
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 242  
Db 108 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 167  
QY 243 HNAKTKPREQYNSTYRVVSVLTVLIHQDLNGKEYCKVSKNKPAPIEKTISKAKGQPR 302  
Db 168 HNAKTKPREQYNSTYRVVSVLTVLIHQDLNGKEYCKVSKNKPAPIEKTISKAKGQPR 227  
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362  
Db 228 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 287  
QY 363 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 404  
Db 288 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPG 329  
RESULT 3  
S69339  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C;Accession: S69339; S72664  
R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A;Reference number: S69339; MUID:95262687; PMID:7744049  
A;Accession: S69339  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <KHA>  
A;Cross-references: EMBL:X81695  
R;Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S72664  
A;Accession: S72664  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140,'C',142-374 <KHA>  
A;Cross-references: EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
Query Match 52.9%; Score 1198; DB 2; Length 374;  
Best Local Similarity 99.1%; Pred. No. 6.9e-67;  
Matches 220; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 242  
Db 152 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 211  
QY 243 HNAKTKPREQYNSTYRVVSVLTVLIHQDLNGKEYCKVSKNKPAPIEKTISKAKGQPR 302  
Db 212 HNAKTKPREQYNSTYRVVSVLTVLIHQDLNGKEYCKVSKNKPAPIEKTISKAKGQPR 271  
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362  
Db 272 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 331

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QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 404
Db 332 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 373

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R: Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 51.3%; Score 1162; DB 2; Length 234;
Best Local Similarity 99.1%; Pred. No. 7e-65;
Matches 214; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
Db 19 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 78

QY 243 HNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 302
Db 79 HNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 138

QY 303 EPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 362
Db 139 EPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 198

QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 398
Db 199 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 234

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R: Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
C:Genetics:
A:Gene: IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q23.3-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 1146.5; DB 2; Length 377;
Best Local Similarity 66.0%; Pred. No. 1e-63;
Matches 227; Conservative 19; Mismatches 33; Indels 65; Gaps 7;

QY 76 CNRTHNRVCEKGRVLEIEF-----CLKHRSC---PPGFGVVQAGTPERTVC 121
Db 83 CNVNH-KPSNTKVDKRVELKPLGDTHTCPRCPKSCDTPPP-----C 126

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: A60764
R: Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmbo, b1, c3, c5, u) with an IGHG4 converted
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 1144.5; DB 2; Length 377;
Best Local Similarity 66.0%; Pred. No. 1.4e-63;
Matches 227; Conservative 19; Mismatches 33; Indels 65; Gaps 7;

QY 76 CNRTHNRVCEKGRVLEIEF-----CLKHRSC---PPGFGVVQAGTPERTVC 121
Db 83 CNVNH-KPSNTKVDKRVELKPLGDTHTCPRCPKSCDTPPP-----C 126

QY 122 KRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNCISGNSBSTQKSGGGGG 180
Db 127 PRCPPEP-KSCDTPPPCPRCPKSCDTP----- 152

QY 181 GGTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240
Db 153 PPFCPRCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 212

QY 241 EVHNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 300
Db 213 EVHNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 272

QY 301 PREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 360
Db 273 PREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 332

QY 361 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 404
Db 333 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 376

RESULT 7
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: G2HU
R: Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmbo, b1, c3, c5, u) with an IGHG4 converted
A:Reference number: G2HU; MUID:90007613; PMID:2571587
A:Accession: G2HU
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 1146.5; DB 2; Length 377;
Best Local Similarity 66.0%; Pred. No. 1e-63;
Matches 227; Conservative 19; Mismatches 33; Indels 65; Gaps 7;

QY 76 CNRTHNRVCEKGRVLEIEF-----CLKHRSC---PPGFGVVQAGTPERTVC 121
Db 83 CNVNH-KPSNTKVDKRVELKPLGDTHTCPRCPKSCDTPPP-----C 126
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QY 122 KRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNCISGNSBSTQKSGGGGG 180
Db 127 PRCPPEP-KSCDTPPPCPRCPKSCDTP----- 152

QY 181 GGTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240
Db 153 PPFCPRCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 212

QY 241 EVHNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 300
Db 213 EVHNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 272

QY 301 PREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 360
Db 273 PREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 332

QY 361 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 404
Db 333 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 376

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: A60764
R: Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmbo, b1, c3, c5, u) with an IGHG4 converted
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 1144.5; DB 2; Length 377;
Best Local Similarity 66.0%; Pred. No. 1.4e-63;
Matches 227; Conservative 19; Mismatches 33; Indels 65; Gaps 7;

QY 76 CNRTHNRVCEKGRVLEIEF-----CLKHRSC---PPGFGVVQAGTPERTVC 121
Db 83 CNVNH-KPSNTKVDKRVELKPLGDTHTCPRCPKSCDTPPP-----C 126

QY 122 KRCPDGFFSNETSSKAP-CRKHTNCSVFGLLLTQKGNATHDNCISGNSBSTQKSGGGGG 180
Db 127 PRCPPEP-KSCDTPPPCPRCPKSCDTP----- 152

QY 181 GGTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240
Db 153 PPFCPRCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 212

QY 241 EVHNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 300
Db 213 EVHNAKTPREEQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG 272

QY 301 PREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 360
Db 273 PREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG 332

QY 361 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 404
Db 333 SFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 376

RESULT 7
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: G2HU
R: Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmbo, b1, c3, c5, u) with an IGHG4 converted
A:Reference number: G2HU; MUID:90007613; PMID:2571587
A:Accession: G2HU
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 1146.5; DB 2; Length 377;
Best Local Similarity 66.0%; Pred. No. 1e-63;
Matches 227; Conservative 19; Mismatches 33; Indels 65; Gaps 7;

QY 76 CNRTHNRVCEKGRVLEIEF-----CLKHRSC---PPGFGVVQAGTPERTVC 121
Db 83 CNVNH-KPSNTKVDKRVELKPLGDTHTCPRCPKSCDTPPP-----C 126
```

Matches 208; Conservative 8; Mismatches 4; Indels 1; G



```
Query Match 40.2%; Score 909; DB 1; Length 323;
Best Local Similarity 72.8%; Pred. No. 3.9e-49;
Matches 163; Conservative 28; Mismatches 31; Indels 2; Gaps 1;

QY 183 TC--PPCPAPELGPGSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 240
D 99 TCSKPTCPPELLGPGSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 158
QY 241 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 300
D 159 QVTRARPLEAQPNSTIRVVSTLPIHQDWLNGKEYKCKVSNKALPAPIEKTISKARG 218
QY 301 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 360
D 219 PLEPKVYTMGPPELSSRSVSLTCMINGFYPSPDISVEWEEKNGKAEDNYKTTTFAVLDSG 278
QY 361 SFELYSKLTVDKSRWQQGNVSCVSMHEALHNNHYTKQSLSPG 404
D 279 SYFLYKLSVPTSWQKGDVFTCSVMHEALHNNHYTKQSLSPG 322

RESULT 11
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
A:Gene: Igc2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 39.9%; Score 902.5; DB 2; Length 328;
Best Local Similarity 59.7%; Pred. No. 1e-48;
Matches 172; Conservative 36; Mismatches 53; Indels 27; Gaps 4;

QY 125 PDGFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGTC 184
D 59 PSGLYSLSSMVTVPASSLSKSY-----TCNVNHPATTTKDKRVGTGTK 103

RESULT 12
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130
A:Gene: Igc2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 900.5; DB 2; Length 277;
Best Local Similarity 60.6%; Pred. No. 1.1e-48;
Matches 172; Conservative 35; Mismatches 58; Indels 19; Gaps 4;

QY 125 PDGFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGTC 184
D 8 PSGLYSLSSMVTVPASSLSKSY-----TCNVNHPATTTKDKRVGTGTK 52

RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130
A:Gene: Igc2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 900.5; DB 2; Length 277;
Best Local Similarity 60.6%; Pred. No. 1.1e-48;
Matches 172; Conservative 35; Mismatches 58; Indels 19; Gaps 4;

QY 125 PDGFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGTC 184
D 8 PSGLYSLSSMVTVPASSLSKSY-----TCNVNHPATTTKDKRVGTGTK 52

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130
A:Gene: Igc2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 900.5; DB 2; Length 277;
Best Local Similarity 60.6%; Pred. No. 1.1e-48;
Matches 172; Conservative 35; Mismatches 58; Indels 19; Gaps 4;

QY 125 PDGFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKSGGGGGGTC 184
D 8 PSGLYSLSSMVTVPASSLSKSY-----TCNVNHPATTTKDKRVGTGTK 52
```

Db 113 HTAQRPKBEQFNSTYRVVSVLPQHODWLNKGFCKVNNKDLPAPIITRIISKAKQTR 172  
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPVLDSDG 360  
Db 173 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPEPGNYRTTTPQDDVDG 232  
QY 361 SPFLYSLKLVTDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404  
Db 233 TYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPG 276

RESULT 14  
G2GP  
Ig gamma-2 chain C region - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004  
C:Accession: A94552; A90359; A90384; A90385; A02151  
R:Trichmann, T.M.  
submitted to the Atlas, April 1975  
A:Reference number: A94553  
A:Accession: A94553  
A:Molecule type: protein  
A:Residues: 1-3 <TRI>  
A:Cross-references: UNIPROT:P01862  
R:Birshtein, B.K.; Huseain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
A:Reference number: A90352; MUID:71058471; PMID:5538606  
A:Accession: A90352  
A:Molecule type: protein  
A:Residues: 4-68 <BIR>  
R:Turner, K.J.; Cebra, J.J.  
Biochemistry 10, 9-17, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
A:Reference number: A90359; MUID:71058486; PMID:5538616  
A:Accession: A90359  
A:Molecule type: protein  
A:Residues: 69-133;312-329 <TR>  
R:Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90384; MUID:75036072; PMID:4429665  
A:Accession: A90384  
A:Molecule type: protein  
A:Residues: 134-226 <TRA>  
R:Trischmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90385; MUID:75036073; PMID:4609467  
A:Accession: A90385  
A:Molecule type: protein  
A:Residues: 227-311 <TR2>  
R:Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
A:Reference number: A90354; MUID:71058474; PMID:4922544  
A:Contents: annotation; disulfide bonds  
A:Note: Cys-16 is involved in a heavy-light chain bond  
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:21-81/Domain: immunoglobulin homology <IM1>  
F:135-204/Domain: immunoglobulin homology <IM2>  
F:241-310/Domain: immunoglobulin homology <IM3>  
F:28-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:248-308/Disulfide bonds: #status experimental

Query Match 39.3%; Score 890.5; DB 1; Length 329;

Best Local Similarity 60.7%; Pred. No. 5.5e-48;  
Matches 170; Conservative 33; Mismatches 64; Indels 13; Gaps 2;  
QY 127 GFPSNETSSKAPCRHTNCSVFGLLLTQKGNATHDNCISGNSESTQKSGGGGGGTCPP 186  
Db 61 GLYSLTSMVTVSSQKATCNVAHPASSTKVDKTVPIRTZPBPC-----TCPK 109  
QY 187 CPAPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 246  
Db 110 CPPPENLGGPSVFIIPPCKKOTLMISLTPRVTCVVVDVSDQDEPEVQFTWFDVNDKPVGNAE 169  
QY 247 TKPREEOYNSTYRVVSVLTVLHODWLNKGFCKVSNKALPAPIEKTISKAKGQPREPOV 306  
Db 170 TKPRVEQYNTTFRVESVLPQHODWLNKGFCKVSNKALPAPIEKTISKAKGAPMPDV 229  
QY 307 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPVLDSDGSFFL 364  
Db 230 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPEPGNYRTTTPQDDVDG 289  
QY 365 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 404  
Db 290 YSKLTVDKSANDQGTVTTCVMHEALHNHYTQKAIKSRSPG 329

RESULT 15  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47158  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03778; NID:G433121; PIDN:AAAS2216.1; PID:G433122  
C:Gene: IgG1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 38.9%; Score 880.5; DB 2; Length 328;  
Best Local Similarity 72.3%; Pred. No. 2.3e-47;  
Matches 162; Conservative 27; Mismatches 32; Indels 3; Gaps 2;  
QY 183 TCPPCPAPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
Db 105 TCPICPGCE-VAGPSVFIPPKPKOTLMISQTPETVCVVVDVSKHAHVQFSWYVDGVEV 163  
QY 243 HNAKTKPREEOYNSTYRVVSVLTVLHODWLNKGFCKVSNKALPAPIEKTISKAKGQPR 302  
Db 164 HTAETRPKEEQFNSTYRVVSVLPQHODWLNKGFCKVSNKALPAPIETRTISKAKGQSR 223  
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTTPVLDSDG 360  
Db 224 EPQVYTLPPPAEELSRSKVTLCVLGVFPYPPDIHVWESNGQPEPEPTVTRTTPPQDDVDG 283

Search completed: March 8, 2005, 14:46:15  
Job time : 17.4652 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 74.6958 Seconds  
(without alignments)  
2769.633 Million cell updates/sec

Title: US-09-389-782A-7  
Perfect score: 2264  
Sequence: 1 EFPFKYLHYDETSQILLC.....VMHEALHNHYTQKSLSPG 404

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1204	53.2	330	1 GCL_HUMAN	P01857 homo sapien
2	1204	53.2	465	2 Q6GMX6	Q6gmx6 homo sapien
3	1204	53.2	466	2 Q6IN78	Q6in78 homo sapien
4	1204	53.2	469	2 Q7Z7P5	Q7z7p5 homo sapien
5	1204	53.2	470	2 Q6PJA4	Q6pja4 homo sapien
6	1204	53.2	470	2 Q7Z5W1	Q7z5w1 homo sapien
7	1204	53.2	472	2 Q6N089	Q6n089 homo sapien
8	1204	53.2	475	2 Q6GMW7	Q6gmw7 homo sapien
9	1204	53.2	476	2 Q6GMX1	Q6gmx1 homo sapien
10	1204	53.2	679	2 Q96PQ8	Q96pq8 homo sapien
11	1200	53.0	473	2 Q6P055	Q6p055 homo sapien
12	1200	53.0	475	2 Q6M2Q6	Q6m2q6 homo sapien
13	1200	53.0	480	2 Q6N094	Q6n094 homo sapien
14	1200	53.0	481	2 Q6N097	Q6n097 homo sapien
15	1200	53.0	482	2 Q7Z351	Q7z351 homo sapien
16	1198	52.9	348	2 Q6PYX1	Q6pyx1 homo sapien
17	1198	52.9	473	2 Q6M2V7	Q6m2v7 homo sapien
18	1198	52.9	478	2 Q6P181	Q6p181 homo sapien
19	1198	52.9	480	2 Q6PJF1	Q6pjf1 homo sapien
20	1198	52.9	544	2 Q6N095	Q6n095 homo sapien
21	1197	52.9	466	2 Q6N096	Q6n096 homo sapien
22	1193	52.7	475	2 Q6N095	Q6n095 homo sapien
23	1187	52.4	487	2 Q652L2	Q652l2 mus sp. fv/
24	1146.5	50.6	354	2 Q86T72	Q86t72 homo sapien
25	1142.5	50.5	521	2 Q8N4Y9	Q8n4y9 homo sapien
26	1141.5	50.4	518	2 Q6N030	Q6n030 homo sapien
27	1137.5	50.2	326	1 GC2_HUMAN	P01859 homo sapien
28	1137.5	50.2	417	2 Q6N093	Q6n093 homo sapien
29	1136.5	50.2	509	2 Q8N17	Q8n17 homo sapien
30	1134.5	50.1	464	2 Q6M2U6	Q6m2u6 homo sapien
31	1133	50.0	327	1 GC4_HUMAN	P01861 homo sapien

32	1133	50.0	473	2 Q8TC63	Q8tc63 homo sapien
33	1132.5	50.0	465	2 Q6P6C4	Q6p6c4 homo sapien
34	1125.5	49.7	290	1 GC3_HUMAN	P01860 homo sapien
35	1124	49.6	476	2 Q6MZX7	Q6mzx7 homo sapien
36	1123.5	49.6	493	2 Q68CN4	Q68cn4 homo sapien
37	1013	44.7	401	1 T11B_HUMAN	Q00300 homo sapien
38	909	40.2	323	1 GC_RABIT	P01870 oryctolagus
39	907	40.1	337	2 Q95M34	Q95m34 equus caball
40	896	39.6	401	2 Q6P112	Q6p112 mus musculus
41	892	39.4	401	1 T11B_MOUSE	O08712 mus musculus
42	890.5	39.3	329	1 GC2_CAVPO	P01862 cavia porce
43	879	38.8	401	1 T11B_RAT	O08727 rattus norv
44	841.5	37.2	329	1 GC3_MOUSE	P22436 mus musculus
45	841.5	37.2	470	2 Q7TWK1	Q7twk1 mus musculus

ALIGNMENTS

RESULT 1  
GCL\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE 19 gamma-1 chain C region.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Sayler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL). AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Sayler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;

RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RL Intrachain disulfide bonds.";  
RN Biochemistry 9:3188-3196(1970).  
RP [7]  
RX DISULFIDE BONDS.  
RA MEDLINE=77070267; PubMed=1002129;  
RT Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the  
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
CC G1M(3) marker and the G1M (non-1) markers.  
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A93433; GHHU  
DR PDB; 1A07; X-ray; H=1-103.  
DR PDB; 1D5B; X-ray; B/H=1-101.  
DR PDB; 1D5I; X-ray; H=1-101.  
DR PDB; 1D6V; X-ray; H=1-101.  
DR PDB; 1DN2; X-ray; A/B=120-326.  
DR PDB; 1E4K; X-ray; A/B=106-329.  
DR PDB; 1FC1; X-ray; A/B=106-329.  
DR PDB; 1FC2; X-ray; D=106-329.  
DR PDB; 1FCC; X-ray; A=121-326.  
DR PDB; 1H2H; X-ray; H/K=1-330.  
DR PDB; 1I72; X-ray; B/D=1-103.  
DR PDB; 1IIS; X-ray; A/B=107-330.  
DR PDB; 1IIX; X-ray; A/B=107-330.  
DR PDB; 1L6X; X-ray; A=120-326.  
DR PDB; 1OQX; X-ray; A=120-326.  
DR PDB; 2RCS; X-ray; H=1-103.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM; 147100; -  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; F:antigen binding; TAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; ig; 3.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW 3D-structure; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT 99 110 Hinge.

FT DOMAIN 111 223  
FT DISULFID 224 330  
FT DISULFID 27 83  
FT DISULFID 103 103 Interchain (with light chain).  
FT DISULFID 109 109 Interchain (with heavy chain).  
FT DISULFID 112 112 Interchain (with heavy chain).  
FT DISULFID 144 204  
FT CARBOHYD 180 180  
FT VARIANT 97 97  
FT N-linked (GlcNAc...).  
FT K -> R (in G1M(3) marker).  
FT /FTid=VAR\_003886.  
FT D -> E (in G1M(non-1) marker).  
FT /FTid=VAR\_003887.  
FT L -> M (in G1M(non-1) marker).  
FT /FTid=VAR\_003888.  
FT VARIANT 239 239  
FT VARIANT 241 241  
FT STRAND 23 24  
FT STRAND 26 33  
FT STRAND 38 38  
FT STRAND 41 41  
FT TURN 42 45  
FT TURN 48 49  
FT STRAND 50 52  
FT STRAND 57 58  
FT TURN 59 61  
FT STRAND 62 71  
FT HELIX 73 75  
FT TURN 76 78  
FT STRAND 82 87  
FT TURN 88 91  
FT STRAND 92 97  
FT TURN 102 103  
FT STRAND 122 126  
FT HELIX 130 134  
FT TURN 136 137  
FT STRAND 141 149  
FT STRAND 157 162  
FT TURN 163 164  
FT STRAND 165 167  
FT STRAND 171 172  
FT STRAND 176 177  
FT TURN 179 180  
FT STRAND 183 190  
FT HELIX 193 197  
FT TURN 198 199  
FT STRAND 202 207  
FT TURN 209 210  
FT STRAND 215 219  
FT STRAND 227 227  
FT STRAND 230 234  
FT STRAND 238 242  
FT STRAND 245 256  
FT STRAND 261 266  
FT TURN 267 268  
FT STRAND 269 270  
FT STRAND 274 276  
FT STRAND 280 281  
FT TURN 283 284  
FT STRAND 287 296  
FT HELIX 297 301  
FT TURN 302 303  
FT STRAND 306 311  
FT TURN 313 314  
FT HELIX 316 318  
FT STRAND 319 324  
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;  
Query Match 53.2%; Score 1204; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 4.2e-71;  
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 183 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
DB 108 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 167

QY 243 HNAKTPREQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPR 302  
 DB 168 HNAKTPREQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPR 227  
 QY 303 EPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 362  
 DB 228 EPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 287  
 QY 363 FLYSKLTVDKSRWQGNVPSFCSVMHEALHNHYTQKSLSLSPG 404  
 DB 288 FLYSKLTVDKSRWQGNVPSFCSVMHEALHNHYTQKSLSLSPG 329

RESULT 2  
 Q6GMX6 PRELIMINARY; PRT; 465 AA.  
 AC Q6GMX6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Casavant T.L., Scheetz T.E.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766; AAH73766.1; -;  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00407; IG; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 465 AA; B3A9B7D0FDB1386E CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-71;

Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 183 TCPPCPAPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
 DB 243 TCPPCPAPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 302  
 QY 243 HNAKTPREQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPR 302  
 DB 303 HNAKTPREQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPR 362  
 QY 303 EPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 362  
 DB 363 EPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 422  
 QY 363 FLYSKLTVDKSRWQGNVPSFCSVMHEALHNHYTQKSLSLSPG 404  
 DB 423 FLYSKLTVDKSRWQGNVPSFCSVMHEALHNHYTQKSLSLSPG 464

RESULT 3  
 Q6IN78 PRELIMINARY; PRT; 466 AA.  
 AC Q6IN78;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGHG1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Casavant T.L., Scheetz T.E.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC072419; AAH72419.1; -;  
 DR HSSP; P01861; 1ADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.

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DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCED81076E CRC64;

Query Match
Best Local Similarity 53.2%; Score 1204; DB 2; Length 466;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
DB 244 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 303
QY 243 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 302
DB 304 HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 363
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSF 362
DB 364 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSF 423
QY 363 FLYSKLTVDSRWQQGNVFCSCVMHEALHNHYTKQSLSPG 404
DB 424 FLYSKLTVDSRWQQGNVFCSCVMHEALHNHYTKQSLSPG 465

RESULT 4
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE iHGI protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSP; P01857; IZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; Igv; 1.

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DR Pfam: PF07654; Cl-set; 3.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGcl; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-71;  
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 242  
 DB 248 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 307  
 QY 243 HNAKTKPREQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 302  
 DB 308 HNAKTKPREQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 367  
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 362  
 DB 368 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 427  
 QY 363 FLYSKLTVDKSRWQGNVFSCSVHHEALHNHYTQKSLSLSPG 404  
 DB 428 FLYSKLTVDKSRWQGNVFSCSVHHEALHNHYTQKSLSLSPG 469

## RESULT 6

Q725W1 PRELIMINARY; PRT; 470 AA.  
 ID Q725W1  
 AC Q725W1  
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udín T.B., Tohiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC053984; AAH53984.1; -;  
 DR HSSP; P01857; 1HZH.

DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG-cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-set; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-71;  
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 242  
 DB 248 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 307  
 QY 243 HNAKTKPREQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 302  
 DB 308 HNAKTKPREQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 367  
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 362  
 DB 368 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 427  
 QY 363 FLYSKLTVDKSRWQGNVFSCSVHHEALHNHYTQKSLSLSPG 404  
 DB 428 FLYSKLTVDKSRWQGNVFSCSVHHEALHNHYTQKSLSLSPG 469

## RESULT 7

Q6N089 PRELIMINARY; PRT; 472 AA.  
 ID Q6N089  
 AC Q6N089  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686P15220.  
 GN Name=DKFZp686P15220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RG The German Human cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640627; CAE45781.1; -;  
 DR HSSP; P01861; 1ADQ  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG-cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-set; 3.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGcl; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-71;  
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 242

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Db 250 TCPPCPAPPELLGGPSVFLPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 309
Qy 243 HNAKTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 302
Db 310 HNAKTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 369
Qy 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 362
Db 370 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 429
Qy 363 FLYSKLTVDKSRWQOQGNVFSCVMHEALHNHYTQKSLSLSPG 404
Db 430 FLYSKLTVDKSRWQOQGNVFSCVMHEALHNHYTQKSLSLSPG 471

RESULT 8
O6GMW7 ID O6GMW7 PRELIMINARY; PRT; 475 AA.
AC O6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG1; 3.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE5D736860F8 CRC64;

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Query Match 53.2%; Score 1204; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 6.4e-71;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 TCPPCPAPPELLGGPSVFLPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
Db 253 TCPPCPAPPELLGGPSVFLPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 312
Qy 243 HNAKTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 302
Db 313 HNAKTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 372
Qy 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 362
Db 373 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 432
Qy 363 FLYSKLTVDKSRWQOQGNVFSCVMHEALHNHYTQKSLSLSPG 404
Db 433 FLYSKLTVDKSRWQOQGNVFSCVMHEALHNHYTQKSLSLSPG 474

RESULT 9
O6GMX1 ID O6GMX1 PRELIMINARY; PRT; 476 AA.
AC O6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 476 AA; 52286 MW; 622AABAS62DDE9D CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-71;  
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
 Db 254 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 313  
 QY 243 HNAKTKPREEQYNSTYRVSVLTVLHQQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 302  
 Db 314 HNAKTKPREEQYNSTYRVSVLTVLHQQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 373  
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 362  
 Db 374 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 433  
 QY 363 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 404  
 Db 434 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 475

RESULT 10  
 Q96P08 PRELIMINARY; PRT; 679 AA.  
 AC Q96P08;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Factor VII active site mutant immunoconjugate.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;  
 RA Hu Z., Garen A.;  
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
 cells for immunotherapy in mouse models of prostatic cancer.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu Z., Garen A.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF272774; AAK58686.2; -.  
 DR HSP; P08709; 1KLI.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000152; Asx hydroxyl S.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001254; Peptidase s1.  
 DR InterPro; IPR009003; Pept Ser\_Cys.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00407; IGC1; 1.

DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLA\_1; 1.  
 DR PROSITE; PS00835; IG\_Like; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW EGF-like domain; Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 53.2%; Score 1204; DB 2; Length 679;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-71;  
 Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
 Db 457 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 516  
 QY 243 HNAKTKPREEQYNSTYRVSVLTVLHQQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 302  
 Db 517 HNAKTKPREEQYNSTYRVSVLTVLHQQDWLNGKEYCKVSNKALPAPIETKISKAKGQPR 576  
 QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 362  
 Db 577 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSF 636  
 QY 363 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 404  
 Db 637 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 678

RESULT 11  
 Q6P055 PRELIMINARY; PRT; 473 AA.  
 AC Q6P055;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC065820; AAH65820.1; --  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;  
  
Query Match 53.0%; Score 1200; DB 2; Length 473;  
Best Local Similarity 99.5%; Pred. No. 1.2e-70;  
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 183 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
Db 251 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 310  
  
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302  
Db 311 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 370  
  
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362  
Db 371 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 430  
  
QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSLSPG 404  
Db 431 FLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSLSPG 472  
  
RESULT 12  
Q6MZQ6 PRELIMINARY; PRT; 475 AA.  
ID Q6MZQ6  
AC Q6MZQ6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFp686G11190.  
GN Name=DKFp686G11190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human cDNA Consortium;  
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640947; CAE45972.1; --  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;  
  
Query Match 53.0%; Score 1200; DB 2; Length 480;  
Best Local Similarity 99.5%; Pred. No. 1.2e-70;  
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 183 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
Db 258 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 317  
  
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302  
Db 318 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 377

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;  
  
Query Match 53.0%; Score 1200; DB 2; Length 475;  
Best Local Similarity 99.5%; Pred. No. 1.2e-70;  
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 183 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
Db 253 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 312  
  
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302  
Db 313 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 372  
  
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 362  
Db 373 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 432  
  
QY 363 FLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSLSPG 404  
Db 433 FLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSLSPG 474  
  
RESULT 13  
Q6N094 PRELIMINARY; PRT; 480 AA.  
ID Q6N094  
AC Q6N094  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFp686O01196.  
GN Name=DKFp686O01196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640622; CAE45776.1; --  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;  
  
Query Match 53.0%; Score 1200; DB 2; Length 480;  
Best Local Similarity 99.5%; Pred. No. 1.2e-70;  
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 183 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242  
Db 258 TCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 317  
  
QY 243 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 302  
Db 318 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 377

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QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSP 362
DB 378 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSP 437
QY 363 FLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 404
DB 438 FLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 479

RESULT 14
Q6N097 PRELIMINARY; PRT; 481 AA.
AC G6N097;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFzp686H20196.
GN Name=DKFzp686H20196;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640619; CAB45773.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 47220D9B64BDF98B CRC64;

Query Match 53.0%; Score 1200; DB 2; Length 481;
Best Local Similarity 99.5%; Pred. No. 1.2e-70;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
DB 259 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 318
QY 243 HNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 302
DB 319 HNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 378
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSP 362
DB 379 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSP 438
QY 363 FLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 404
DB 439 FLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 480

RESULT 15
Q7Z351 PRELIMINARY; PRT; 482 AA.
AC Q7Z351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Hypothetical protein DKFzp686N02209.
GN Name=DKFzp686N02209;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; IZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 53.0%; Score 1200; DB 2; Length 482;
Best Local Similarity 99.5%; Pred. No. 1.2e-70;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 242
DB 260 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 319
QY 243 HNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 302
DB 320 HNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 379
QY 303 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSP 362
DB 380 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSP 439
QY 363 FLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 404
DB 440 FLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPG 481

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Search completed: March 8, 2005, 14:44:40  
Job time : 75.6958 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:11 ; Search time 84.1064 Seconds  
(without alignments)  
1843.986 Million cell updates/sec

Title: US-09-389-782A-8  
Perfect score: 2246  
Sequence: 1 MKTHTCPCPAPPELLGGPS.....QKGNATHDNCISGSESTOK 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2246	100.0	401	4	AAB80904 Human met
2	2246	100.0	401	4	AAY72922 Human met
3	1271.5	56.6	613	8	ADR46827 Human bet
4	1271.5	56.6	861	7	ADG76139 Human NOV
5	1271.5	56.6	861	8	ADF45362 Human sem
6	1271.5	56.6	861	8	ADO40296 Human sem
7	1271.5	56.6	878	8	ADG76141 Human NOV
8	1271.5	56.6	878	8	ADF45364 Human sem
9	1271.5	55.9	409	7	ADO40298 Human sem
10	1254.5	55.9	409	7	ADP75170 Fusion co
11	1249	55.6	731	4	AAMS2156 Humanised
12	1249	55.6	741	4	AAMS2159 Humanised
13	1244	55.4	412	7	ADP75168 Fusion co
14	1241	55.3	489	7	ADC98610 Human ang
15	1240	55.2	248	3	AAB17951 FC-TNP-al
16	1240	55.2	248	5	ABB73419 FC-TNP-al
17	1239	55.2	652	2	AAW48650 Heavy cha
18	1239	55.2	406	7	ADP75162 Fusion co
19	1239	55.2	409	7	ADP75176 Fusion co
20	1239	55.2	410	7	ADP75166 Fusion co
21	1239	55.2	412	7	ADP75164 Fusion co
22	1239	55.2	416	7	ADP75160 Fusion co
23	1239	55.2	422	7	ADP75174 Fusion co
24	1239	55.2	450	7	ADP75172 Fusion co
25	1238	55.1	228	3	AAY96529 Human IGG

26	1238	55.1	228	3	AAB16955 Human IGG
27	1238	55.1	228	4	AAB98953 Human IGG
28	1238	55.1	228	5	ABB04279 Human IGG
29	1238	55.1	228	5	AAU81074 Human IGG
30	1238	55.1	228	5	AAE14310 Human imm
31	1238	55.1	228	5	ABB73410 Human imm
32	1238	55.1	228	5	AAE66012 Human imm
33	1238	55.1	228	5	AAU73018 Human imm
34	1238	55.1	228	6	ABJ38267 Human IGG
35	1238	55.1	228	7	ADN59683 Human IGG
36	1238	55.1	228	8	ADM17708 Human IGG
37	1238	55.1	228	8	ADQ75329 Human IGG
38	1238	55.1	243	3	AAB17957 FC-MMP in
39	1238	55.1	243	5	ABB73425 FC-MMP in
40	1238	55.1	243	7	ADN59746 Vector 20
41	1238	55.1	247	3	AAB16958 FC-TMP pr
42	1238	55.1	247	5	ABB73411 FC-TPO mi
43	1238	55.1	248	3	AAB17953 FC-IL-1 a
44	1238	55.1	248	5	ABB73421 FC-interl
45	1238	55.1	250	7	ADD31616 Ang-2 pep

ALIGNMENTS

RESULT 1  
AAB80904  
ID AAB80904 standard; protein; 401 AA.  
XX AAB80904;  
AC AAB80904;  
XX 31-MAY-2001 (first entry)  
DE Human metFcDeltaC-OPG(22-194) fusion protein.

Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;  
multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;  
osteoclast formation inhibition; bone resorption inhibition;  
immunoglobulin.

OS Homo sapiens.  
XX WO200117543-A2.  
XX 15-MAR-2001.  
XX 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.  
XX (AMGE-) AMGEN INC.  
XX Dunstan CR;  
XX WPI; 2001-265936/27.  
XX Preventing or treating lytic bone diseases, particularly associated with cancer or metastasis, by administering an osteoprotegrin polypeptide.

XX Claim 11; Fig 8; 87pp; English.  
XX The present invention relates to a method for the prevention or treatment of lytic bone disease or multiple myeloma. Also the method can be used for preventing metastasis of cancer to bone or osteosclerotic bone metastasis. The method comprises administering an OPG (osteoprotegrin) polypeptide or OPG fusion protein. The present sequence is one such OPG fusion protein. OPG inhibits formation of osteoclasts (and thus bone resorption) by blocking differentiation from monocytes/macrophage precursors. The OPG polypeptide can be used in a method of preventing or treating lytic bone disease, for preventing metastasis of cancer to bone (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal, rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal tract, multiple myeloma or lymphoma) and preventing the osteosclerotic

CC bone metastasis. The OPG fusion polypeptides are used in the prevention  
 CC or treatment of loss of bone mass, which occurs in conditions including  
 CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis  
 CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and  
 CC congenital forms of osteoporosis (osteogenesis imperfecta,  
 CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis  
 CC due to immobilisation of extremities; Paget's disease of bone (osteitis  
 CC deformans) in adults and juveniles; osteomyelitis, or an infectious  
 CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung  
 CC and kidney) and haematological malignancies (multiple myeloma, lymphoma and  
 CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with  
 CC parathyroidism and renal function disorders; osteopaenia following  
 CC surgery, induced by steroid administration, and associated with disorders  
 CC of the small and large intestine and with chronic hepatic and renal  
 CC diseases; osteonecrosis, or bone cell death, associated with traumatic  
 CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle  
 CC cell anaemia, systemic lupus erythematosus and other conditions; bone  
 CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;  
 CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins  
 CC are also used in the replacement of structurally sound bone with  
 CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)  
 CC in adults and juveniles; hyperparathyroidism, in congenital bone  
 CC disorders such as fibrous dysplasia, and in osteosclerotic bone  
 CC metastases. The OPG fusion proteins can exhibit increased circulating  
 CC half-lives and slower clearance times, thereby providing a more sustained  
 CC activity. The OPG fusion protein comprises a fragment of the human OPG  
 CC protein and the Fc region of immunoglobulin IgGammal (the hinge, CH2 and  
 CC CH3 regions; see AAB80897-8)

XX  
 SQ Sequence 401 AA;

Query Match 100.0%; Score 2246; DB 4; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-140;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
 DB 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
 QY 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
 DB 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
 QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180  
 DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180  
 QY 301 KQECNRNTHRVCEKGRVLEIFCLKHSRCPGFGVQAGTPPRTVCKCPDGFPPNE 360  
 DB 301 KQECNRNTHRVCEKGRVLEIFCLKHSRCPGFGVQAGTPPRTVCKCPDGFPPNE 360  
 QY 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQK 401  
 DB 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNSESTQK 401

## RESULT 2

AA72922  
 ID AAY72922 standard; protein; 401 AA.  
 XX  
 AC AAY72922;  
 XX  
 DT 13-JUN-2001 (first entry)  
 XX  
 DE Human met-Fc (lacking 1-5 residues)-OPG (22-194 aa) fusion protein.

XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 KW periodontal.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT 1..228  
 FT /note= Met-human IgG1 Fc region lacking 1-5 residues;  
 FT Corresponds to 6-231 residues of human IgG1 Fc region  
 FT 229..401  
 FT Region /note= "Derived from human osteoprotegerin fragment (22-  
 FT 194 residues)"  
 XX WO200118203-A1.  
 XX 15-MAR-2001.  
 XX 18-AUG-2000; 2000WO-US022797.  
 XX 03-SEP-1999; 99US-00389782.  
 XX (AMGE-) AMGEN INC.  
 XX Dunstan CR, Wooden SK, Mann MB;  
 XX WPI; 2001-244572/25.  
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
 XX by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 XX Claim 7; Fig 8; 119pp; English.  
 XX The present sequence is a fusion protein comprising human met-Fc region  
 CC (lacking 1-5 residues) which is fused with a sequence derived from human  
 CC osteoprotegerin (OPG; 22-194 residues) by a linker. OPG negatively  
 CC regulates the formation of osteoclasts in vitro and in vivo. It blocks  
 CC the differentiation of osteoclasts from monocyte or macrophage precursors  
 CC and the reabsorption of bone. The OPG-Fc fusion protein is administered  
 CC for the treatment of bone loss resulting from osteoporosis, Paget's  
 CC disease, osteomyelitis, hypercalcaemia, osteopenia associated with  
 CC surgery or steroid administration, osteonecrosis, bone loss due to  
 CC rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or  
 CC prosthetic loosening

XX  
 SQ Sequence 401 AA;

Query Match 100.0%; Score 2246; DB 4; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-140;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
 DB 1 MDKTHCTPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
 QY 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
 DB 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
 QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180  
 DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180  
 QY 181 SDGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGKETPPPKYLHYDE 240  
 DB 181 SDGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGKETPPPKYLHYDE 240  
 QY 241 ETSHQLLCDKCPPTGYLKHCTAKWKTVCAPCPDHYTSDSWHTSDECLYCSVPCKELQVY 300  
 DB 241 ETSHQLLCDKCPPTGYLKHCTAKWKTVCAPCPDHYTSDSWHTSDECLYCSVPCKELQVY 300

QY 301 KQSCNTHNRVCKEGRYLEIEFCLKHSRCPGFGVVOAGTPTNVTCKRCDPGFSNE 360  
 DB 301 KQSCNTHNRVCKEGRYLEIEFCLKHSRCPGFGVVOAGTPTNVTCKRCDPGFSNE 360  
 QY 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNCISGNSSESTOK 401  
 DB 361 TSSKAPCRKHTNCSVFGLLLTQGNATHDNCISGNSSESTOK 401

## RESULT 3

ADR46827  
 ID ADR46827 standard; protein; 613 AA.

AC ADR46827;  
 XX

DT 18-NOV-2004 (first entry)  
 XX

DE Human betahCG-B11 molecular conjugate protein SEQ ID NO:10.

KW molecular conjugate; monoclonal antibody; human antigen presenting cell;  
 KW antigen presenting cell; APC; human; beta human chorionic gonadotropin;  
 KW betahCG; beta chorionic gonadotropin; antibody;  
 KW T cell-mediated immune response; immunisation; cytostatic; antimicrobial;  
 KW immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;  
 KW CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;  
 KW melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;  
 KW antibody B11; betahCG-B11 molecular conjugate; fusion protein.

XX Homo sapiens.  
 OS Synthetic.

XX WO2004074432-A2.

PN 02-SEP-2004.

XX 30-JAN-2004; 2004WO-US0002725.

PR 31-JAN-2003; 2003US-0443979P.

XX (WEDA-) MEDAREX INC.

PI Keler T, Endres M, He L, Ramakrishna V;  
 XX WPI; 2004-635555/61.

DR N-PSDB; ADR46826.

XX New molecular conjugate having a monoclonal antibody that binds to human  
 PT APCs linked to a beta human chorionic gonadotropin, useful for inducing a  
 PT cytotoxic T cell response in cancers and infectious diseases.

XX Example 1; SEQ ID NO 10; 82pp; English.

XX The present invention describes a molecular conjugate comprising a  
 CC monoclonal antibody that binds to human antigen presenting cells (APCs)  
 CC linked to beta human chorionic gonadotropin (betahCG), where the antibody  
 CC comprises a heavy and/or light chain variable region derived from a human  
 CC VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences  
 CC of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also  
 CC described: (1) a molecular conjugate comprising a human antibody heavy  
 CC chain and a human antibody light chain, where either or both chains are  
 CC linked to betahCG; (2) a molecular conjugate comprising a human single  
 CC chain antibody that binds to human APCs linked to betahCG, where the  
 CC conjugate comprises the 411 amino acid sequence of SEQ ID NO:12  
 CC as described above, and a carrier, optionally in combination with an  
 CC adjuvant; (4) inducing or enhancing a T cell-mediated immune response,  
 CC against betahCG, comprising contacting any of the molecular conjugates  
 CC described above with APCs such that the antigen is processed and  
 CC presented to T cells in a manner which induces or enhances a T cell-  
 CC mediated response against the antigen; (5) immunising a subject  
 CC comprising administering any of the molecular conjugates described above,  
 CC optionally in combination with an adjuvant, a cytokine which stimulates

CC proliferation of dendritic cells and/or an immunostimulatory agent; and  
 CC (6) inducing or enhancing a cytotoxic T cell response against an antigen,  
 CC comprising forming a conjugate of the antigen and a monoclonal antibody  
 CC which binds to APCs, and contacting the conjugate either in vivo or ex  
 CC vivo with APCs such that the antigen is internalised, processed and  
 CC presented to T cells in a manner which induces or enhances a cytotoxic T  
 CC cell response against the antigen. The molecular conjugate has  
 CC cytostatic, antimicrobial, immunosuppressive, anti-HIV, hepatotropic,  
 CC virucide and antimalarial activities, and can be used as a CD8 agonist,  
 CC and in vaccines. The methods and compositions of the present invention  
 CC are useful for inducing a cytotoxic T cell response, and in particular  
 CC for treating autoimmune disorders, cancers and infectious diseases by  
 CC eliciting a potent antigen-specific cytotoxic T lymphocyte response,  
 CC including melanoma, fibrosarcoma, leukaemia, HIV, hepatitis, malaria, and  
 CC herpes. The present sequence represents a human betahCG-B11 molecular  
 CC conjugate, which is used in the exemplification of the present invention.

XX  
 SQ Sequence 613 AA;

Query Match 56.6%; Score 1271.5; DB 8; Length 613;  
 Best Local Similarity 66.6%; Pred. No. 1.4e-75;  
 Matches 259; Conservative 18; Mismatches 53; Indels 59; Gaps 8;

QY 2 DKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
 DB 239 DKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 298  
 QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
 DB 299 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 358  
 QY 122 GQPRSPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLD 181  
 DB 359 GQPRSPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLD 418  
 QY 182 DGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNYHTQKLSLSLSPCKETFPKPKYLHYD 241  
 DB 419 DGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNYHTQKLSLSLSPCKETFPKPKYLHYD 467  
 QY 242 TSHQLLCKDCPP--GTYLKQH-----CTAKWKTVCAPCPDHYTDSWHTSDECLYSPVC 294  
 DB 468 SSKEPLRPRCPINATLAVEKSGCPVITVNTICAG-----YCPMT 510  
 QY 295 KELQVYKQECNTHNRVCKEGRYLEIEFCLKHSRCPGFGVVOAGTPTNVTCKRC 351  
 DB 511 RVLQGLPALPQV--VCNRYDRVPESIRL----PGCPRGVNPVWSYVALSCQCALCRR 563  
 QY 352 -----CPDGFFSNETSSKAP 366  
 DB 564 STTDCGGPKDHPDLCDDPRFQDSSSSSKAP 592

## RESULT 4

ADR76139

ID ADR76139 standard; protein; 861 AA.

XX ADR76139;

XX 11-MAR-2004 (first entry)

XX Human NOVX protein to treat human pathological conditions (SeqID 52).  
 DE human; NOVX; metabolic disorder; diabetes; anorexia; cancer;  
 XX human; NOVX; metabolic disorder; diabetes; anorexia; cancer;  
 KW cardiovascular; infectious; neurodegenerative; immune;  
 KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;  
 KW antiinflammatory; neuroprotective; antilipaeamic; anabolic; cardiant;  
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic.

XX Homo sapiens.

XX WO2003085096-A2.

PN

16-OCT-2003.

01-APR-2003; 2003WO-US009929.

01-APR-2002; 2002US-0368996P.

04-APR-2002; 2002US-0369980P.

05-APR-2002; 2002US-0370381P.

08-APR-2002; 2002US-0370969P.

09-APR-2002; 2002US-0371002P.

12-APR-2002; 2002US-0372002P.

30-MAY-2002; 2002US-0384297P.

07-JUN-2002; 2002US-0386816P.

13-JUN-2002; 2002US-0389123P.

09-AUG-2002; 2002US-0402207P.

24-OCT-2002; 2002US-0420860P.

31-MAR-2003; 2003US-00403676.

(CURA-) CURAGEN CORP.

Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ;  
Edinger SR, Gerlach VL, Grosse WM, Guo X, Gusev VY, Ji W;  
Larochelle WJ, Lepley DM, Li L, Liu X, Macdougall JR, Malyankar UM;  
Millet I, Padigaru M, Patturajan M, Peyman JA, Rastelli L;  
Rieger DK, Rothenberg ME, Shinkets RA, Stone DJ, Taupier RJ;  
Vernet CAM, Zerhusen BD;

WPI; 2003-812726/76.

N-PSDB; ADG76138.

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.

Claim 1; SEQ ID NO 52; 324pp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating metabolic disorders, diabetes, anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune and haematopoietic diseases as well as various dyslipidaemias. Accordingly, these molecules have many activities including anorectic, virucide, nootropic, antiinflammatory, neuroprotective, antilipemic, anabolic and cardiac. Furthermore, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a human NOVX protein of the invention.

Sequence 861 AA;

Query Match 56.6%; Score 1271.5; DB 7; Length 861;  
Best Local Similarity 63.8%; Pred. No. 2.1e-75;  
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKHTCCPCPAPELGGSVFLFPKPKDMLMISTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Db 1 DKHTCCPCPAPELGGSVFLFPKPKDMLMISTPEVTCVVVDVSHEDPEVKFNWYVD 60  
QY 62 GVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
Db 61 GVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120  
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181

Db 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180  
QY 182 DGSFELYSLTVDKSRWQGNVFSVMEALHNNHYTKSLSPGK-----ETFPDPK 234  
Db 181 DGSFELYSLTVDKSRWQGNVFSVMEALHNNHYTKSLSPGKGGGGGGGFPF- 239  
QY 235 YLHYDEE---TSHQLLCKCPGTYLKQH-----CTAKWK-----TVC 269  
Db 240 ----DSEPISSH-----GNTKYQYFVGHKPGNTTORHLDIQIMIMNGTLY 286  
QY 270 APCPDHYT---DSWHTSDECLYCSPVCKELQYVKQECNTRNRYCEK-EGRYLE---- 321  
Db 287 TAARDHIYTVDTIDTSTTEE--IYCS---KLTWKSROAD-----VDTCRMKGKHDECHN 336  
QY 322 -LEFCLKHSRCPGPGVGVQAGTPERNVTYKRC-----PDGFFSNETSKAPC---RHT 371  
Db 337 FIKVLLKQND---DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCPYDAKHA 389  
QY 372 NCSVF 376  
Db 390 NVALF 394  
RESULT 5  
ADF45362  
ID ADF45362 standard; protein; 861 AA.  
XX  
AC ADF45362;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human semaphorin-like protein NOV2t protein SEQ ID NO:52.  
XX  
KW cell migration inhibition; semaphorin-like protein;  
KW angiogenesis inhibition; actin filament formation inhibition;  
KW angiogenic related disorder; cytostatic; gene therapy; cancer;  
KW neuroblastoma; renal carcinoma; fibrosarcoma; rhabdosarcoma cell;  
KW pancreatic cancer; human.  
OS Homo sapiens.  
XX  
PN WO2003102584-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 30-MAY-2003; 2003WO-US017412.  
XX  
PR 30-MAY-2002; 2002US-0384798P.  
PR 09-AUG-2002; 2002US-0402407P.  
PR 28-JAN-2003; 2003US-0443062P.  
PR 31-MAR-2003; 2003US-00403676.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochelle WJ;  
PI Lichenstein HS, Li L, Ooi CE, Padigaru M, Shinkets RA, Zhong M;  
XX  
DR WPI; 2004-035474/03.  
DR N-PSDB; ADF45361.  
PT  
PT Inhibiting cell migration, useful in diagnosing and treating disorders such as cancer, e.g. neuroblastoma, renal carcinoma, fibrosarcoma or rhabdosarcoma, by contacting a cell with a composition comprising NOVX polypeptide.  
XX  
PS Claim 1; SEQ ID NO 52; 197pp; English.  
XX  
CC The present invention describes a method for inhibiting cell migration which comprises contacting a cell with a composition comprising a polypeptide (I) having at least 95% sequence identity to any of the 22 sequences of 17-1047 amino acids (SVEN SEQ ID NOS: 14-56) or any of the 22 sequences of 51-4250 base pairs (ODD SEQ ID NOS: 13-55) defined in the specification, where (I) is a semaphorin-like protein. Also described:

CC (1) a method of inhibiting angiogenesis of a tissue; (2) a method of  
CC inhibiting actin filament formation in a cell; (3) a method of preventing  
CC or alleviating a symptom of an angiogenic related disorder; (4) a  
CC chimeric protein comprising a first polypeptide (1) and second  
CC polypeptide; and (5) a composition comprising a sequence of 649 or 878  
CC amino acids (see ADF45360 or ADF45364). (1) has cytostatic activity, and  
CC can be used in gene therapy. The method is useful for inhibiting cell  
CC migration. (1) and the polynucleotides encoding them can be used in  
CC diagnosing and treating disorders such as cancer, e.g. neuroblastoma,  
CC renal carcinoma, fibrosarcoma, rhabdomyosarcoma cell or a pancreatic cancer.  
CC The present sequence is used in the exemplification of the present  
CC invention.

XX  
SQ Sequence 861 AA;

Query Match 56.6%; Score 1271.5; DB 8; Length 861;  
Best Local Similarity 63.8%; Pred. No. 2.1e-75;  
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61

DB 1 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121

DB 61 GVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181

DB 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 182 DGSFFLYSKLTVDKSRWQQGNVSCSWMEALHNHYTKLSLSPGK-----ETFPKP 234

DB 181 DGSFFLYSKLTVDKSRWQQGNVSCSWMEALHNHYTKLSLSPGKGGGGGGGPPPE- 239

QY 235 YLHDEE---TSQLLCDKCPGTYLKQH-----CTAKWK-----TVC 269

DB 240 ----DSEPIISH-----GNYTKQYVFGVGHKPGRTTQRHLDIQIMIMNGTLY 286

QY 270 APCPDHYIT---DSWHTSDECLYCSPVKELQYVQECNTRNRCVCK-EGRYLE---- 321

DB 287 IAARDHIYTVIDTSHTEE--IYCS---KGLTWKSRQAD-----VDTCRMKGKHKBCHN 336

QY 322 -ISFCLKHSRCPGFGVQAGTERTNVTCKRC-----PDGFFSNETSSKAPC---RKHT 371

DB 337 FIKVLLKKND----DALFVCGTNAFNPSCRNYKMDTLEP---FGDFSGMARCPCYDAKHA 389

QY 372 NCSVF 376

DB 390 NVALF 394

#### RESULT 6

AD040296

ID AD040296 standard; protein; 861 AA.

XX AC AD040296;

XX 15-JUL-2004 (first entry)

XX Human semaphorin-like protein NOV2t.

XX Human; semaphorin; NOV2; angiogenesis inhibitor; gene therapy;

XX cell migration; angiogenesis; actin filament formation;

XX angiogenic-related disorder; loss of balance; weight loss; slow speech;

XX jaundice; fatigue; pain; blood in urine; anaemia; swollen bone; cancer;

XX pancreatic cancer; renal cancer; neuroblastoma; wound healing;

XX tissue regeneration.

XX Homo sapiens.

XX US2004018977-A1.

PN

XX

PD 29-JAN-2004.

XX 30-MAY-2003; 2003US-0049548.

XX 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-00520781.

PR 09-APR-2002; 2002US-0371002P.

PR 30-MAY-2002; 2002US-0384798P.

PR 09-AUG-2002; 2002US-0402407P.

PR 28-JAN-2003; 2003US-0443062P.

PR 31-MAR-2003; 2003US-00403676.

XX (ALVA/) ALVAREZ E.

PA (ANDE/) ANDERSON D W.

PA (DHAN/) DHANABAL M.

PA (KHRA/) KHRAMTSOV N V.

PA (LARO/) LAROCHELLE W J.

PA (LICH/) LICHENSTEIN H S.

PA (LILL/) LI L.

PA (OOIC/) OOI C E.

PA (PADL/) PADIGARU M.

PA (SHIM/) SHIMKETS R A.

PA (ZHON/) ZHONG M.

XX Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochelle WJ;

PI Lichenstein HS, Li L, Ooi CE, Padigaru M, Shimkets RA, Zhong M;

XX WPI; 2004-122082/12.

DR N-PSDB; ADO40295.

XX Inhibiting cell migration, angiogenesis of a tissue or actin filament

PT formation in a cell, for preventing or treating cancer, e.g. renal

PT cancer, comprises contacting or introducing a semaphorin-like polypeptide

PT or nucleic acid.

XX Claim 1; SEQ ID NO 52; 227pp; English.

CC The invention relates to inhibiting cell migration, angiogenesis of a

CC tissue or actin filament formation in a cell comprising contacting the

CC cell with a composition comprising a semaphorin-like polypeptide having

CC at least 95 % sequence identity to any one of 22 NOV2 (NOVa-NOVU)

CC proteins (appearing as ADO40258, ADO40260, ADO40262, ADO40264, . . . etc to

CC ADO40300), or introducing to a cell a composition comprising a nucleic

CC acid having at least 95 % sequence identity to any one of the 22 nucleic

CC acids encoding the NOV2 proteins (appearing as ADO40257, ADO40259,

CC ADO40261, ADO40263, . . . etc to ADO40299). Also included are preventing or

CC administering to a subject an angiogenic-related disorder comprising

CC a polypeptide cited above, a chimeric protein comprising a first

CC polypeptide comprising a NOV2 polypeptide and second polypeptide, and a

CC composition comprising a NOV2s (ADO40294) or NOV2u (ADO40298). The

CC semaphorin-like proteins or nucleic acids are useful for inhibiting cell

CC migration, angiogenesis of a tissue or actin filament formation, or for

CC diagnosing, preventing and treating an angiogenic-related disorder (with

CC symptoms such as loss of balance, weight loss, slow speech, jaundice,

CC fatigue, pain, blood in urine, anaemia or swollen bones) such as cancer,

CC e.g. pancreatic cancer, renal cancer or neuroblastoma, wound healing and

CC tissue regeneration. The nucleic acid may be used in gene therapy. The

CC present sequence represents a NOV2, semaphorin-like protein.

XX Sequence 861 AA;

Query Match 56.6%; Score 1271.5; DB 8; Length 861;

Best Local Similarity 63.8%; Pred. No. 2.1e-75;

Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61

DB 1 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121

DB 61 GVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

Qy 122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPNNTKTPPVLDL 181  
Db 121 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPNNTKTPPVLDL 180  
Qy 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK-----ETFPK 234  
Db 181 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGKGGGGGGGFPF- 239  
Qy 235 YLHYDEE---TSHQLLCKDPCPGTYLKQH-----CTAKWK-----TVC 269  
Db 240 ----DSEPIISH-----GNYTKQYPVFVGHKPGRNTTQRHRLDIQIMIMNGTLY 286  
Qy 270 APCPDHYVT---DSWHTSDECLYCSPVKELQVYKQSCNRTHNRVCECK-EGRYLE---- 321  
Db 287 IAARDHIYTVDDIDTSHTEE---IYCS---KKLTWKSQAD-----VDCRMKGKHDECHN 336  
Qy 322 -IEFCLKHSRCPGFGVVGAGTPERNTVCRC-----PDGFFSNSTSSKAPC---RKHT 371  
Db 337 FIKVLLKND-----DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCYPDAKHA 389  
Qy 372 NCSVF 376  
Db 390 NVALF 394

RESULT 7  
ID ADG76141  
AC ADG76141 standard; protein; 878 AA.  
XX ADG76141;

DT 11-MAR-2004 (first entry)

DE Human NOVX protein to treat human pathological conditions (SeqID 54).

XX human; NOVX; metabolic disorder; diabetes; anorexia; cancer;  
KW cardiovascular; infectious; neurodegenerative; immune;  
KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;  
KW antiinflammatory; neuroprotective; antilipaeamic; anabolic; cardiac;  
KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomic.

XX Homo sapiens.

PN WO2003085096-A2.

XX 16-OCT-2003.

PF 01-APR-2003; 2003WO-US009929.

XX 01-APR-2002; 2002US-0368996P.

PR 04-APR-2002; 2002US-0369980P.

PR 05-APR-2002; 2002US-0370381P.

PR 08-APR-2002; 2002US-0370969P.

PR 09-APR-2002; 2002US-0371002P.

PR 12-APR-2002; 2002US-0372002P.

PR 30-MAY-2002; 2002US-0384297P.

PR 07-JUN-2002; 2002US-0386816P.

PR 13-JUN-2002; 2002US-0389123P.

PR 09-AUG-2002; 2002US-0402207P.

PR 24-OCT-2002; 2002US-0420860P.

PR 31-MAR-2003; 2003US-00403676.

XX (CURA-). CURAGEN CORP.

PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ;  
PI Edinger SR, Gerlach VL, Grosse WM, Guo X, Gusev YV, Ji W;  
PI Larochele WJ, Lepley DM, Li L, Liu X, Macdougall JR, Malyankar UM;  
PI Millet I, Padigaru M, Patturajan M, Peyman JA, Rastelli L;  
PI Rieger DK, Rothenberg ME, Shinkets RA, Stone DJ, Taupier RJ;  
PI Vernet CAM, Zerhusen BD;

DR WPI; 2003-812726/76.  
XX N-PSDB; ADG76140.  
PT New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
PT asthma, or infections.  
XX  
PS Claim 1; SEQ ID NO 54; 324pp; English.  
XX  
CC This invention relates to a novel nucleic acids, and encoded polypeptides  
CC thereof, which have properties related to the stimulation of biochemical  
CC or physiological responses in a cell, tissue, organ or organism.  
CC Specifically, it refers to the use of biologically active fragments for  
CC diagnostic and prognostic assays and furthermore in the treatment of  
CC diverse pathological conditions. The present invention describes novel  
CC human and murine NOVX proteins, as well as methods to modulate their  
CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
CC manufacture of a medicament for treating metabolic disorders, diabetes,  
CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
CC and haematopoietic diseases as well as various dyslipidaemias.  
CC Accordingly, these molecules have many activities including anorectic,  
CC virucide, nootropic, antiinflammatory, neuroprotective, antilipaeamic,  
CC anabolic and cardiac. Furthermore, they are useful in screening assays  
CC to identify small molecules that modulate or inhibit, for example,  
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
CC used as in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. This polypeptide is a human NOVX protein of the  
CC invention.  
XX  
SQ Sequence 878 AA;

Query Match 56.6%; Score 1271.5; DB 7; Length 878;  
Best Local Similarity 63.8%; Pred. No. 2.1e-75;  
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

Qy 2 DKHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61  
Db 1 DKHTCCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVD 60  
Qy 62 GVEVHNATKPREQYNSYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
Db 61 GVEVHNATKPREQYNSYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120  
Qy 122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPNNTKTPPVLDL 181  
Db 121 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPNNTKTPPVLDL 180  
Qy 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK-----ETFPK 234  
Db 181 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGKGGGGGGGFPF- 239  
Qy 235 YLHYDEE---TSHQLLCKDPCPGTYLKQH-----CTAKWK-----TVC 269  
Db 240 ----DSEPIISH-----GNYTKQYPVFVGHKPGRNTTQRHRLDIQIMIMNGTLY 286  
Qy 270 APCPDHYVT---DSWHTSDECLYCSPVKELQVYKQSCNRTHNRVCECK-EGRYLE---- 321  
Db 287 IAARDHIYTVDDIDTSHTEE---IYCS---KKLTWKSQAD-----VDCRMKGKHDECHN 336  
Qy 322 -IEFCLKHSRCPGFGVVGAGTPERNTVCRC-----PDGFFSNSTSSKAPC---RKHT 371  
Db 337 FIKVLLKND-----DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCYPDAKHA 389  
Qy 372 NCSVF 376  
Db 390 NVALF 394

RESULT 8  
ADF45364  
ID ADF45364 standard; protein; 878 AA.

XX ADP45364;  
 AC 26-FEB-2004 (first entry)  
 XX Human semaphorin-like protein NOV2u protein SEQ ID NO:54.  
 DE cell migration inhibition; semaphorin-like protein;  
 XX angiogenesis inhibition; actin filament formation inhibition;  
 KW angiogenic related disorder; cytosatic; gene therapy; cancer;  
 KW neuroblastoma; renal carcinoma; fibrosarcoma; rhabdosarcoma cell;  
 KW pancreatic cancer; human.  
 XX Homo sapiens.  
 OS WO2003102584-A2.  
 XX 11-DEC-2003.  
 PN 30-MAY-2003; 2003WO-US017412.  
 PP 30-MAY-2002; 2002US-0384798P.  
 PR 09-AUG-2002; 2002US-0402407P.  
 PR 28-JAN-2003; 2003US-0443062P.  
 PR 31-MAR-2003; 2003US-00403676.  
 XX (CURA-) CURAGEN CORP.  
 PA Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochele WJ;  
 PI Lichenstein HS, Li L, Ooi CE, Padigar M, Shimkets RA, Zhong M;  
 XX WPI; 2004-035474/03.  
 DR N-PSDB; ADF45363.  
 XX Inhibiting cell migration, useful in diagnosing and treating disorders  
 PT such as cancer, e.g. neuroblastoma, renal carcinoma, fibrosarcoma or  
 PT rhabdosarcoma, by contacting a cell with a composition comprising NOVX  
 PT polypeptide.  
 XX Claim 1; SEQ ID NO 54; 197pp; English.  
 XX The present invention describes a method for inhibiting cell migration  
 CC which comprises contacting a cell with a composition comprising a  
 CC polypeptide (I) having at least 95% sequence identity to any of the 22  
 CC sequences of 17-1047 amino acids (SVEN SEQ ID NOS: 14-56) or any of the  
 CC 22 sequences of 51-4250 base pairs (ODD SEQ ID NOS: 13-55) defined in the  
 CC specification, where (I) is a semaphorin-like protein. Also described:  
 CC (1) a method of inhibiting angiogenesis of a tissue; (2) a method of  
 CC inhibiting actin filament formation in a cell; (3) a method of preventing  
 CC or alleviating a symptom of an angiogenic related disorder; (4) a  
 CC chimeric protein comprising a first polypeptide (I) and second  
 CC polypeptide; and (5) a composition comprising a sequence of 649 or 878  
 CC amino acids (see ADF45360 or ADF45364). (I) has cytostatic activity, and  
 CC can be used in gene therapy. The method is useful for inhibiting cell  
 CC migration. (I) and the polynucleotides encoding them can be used in  
 CC diagnosing and treating disorders such as cancer, e.g. neuroblastoma,  
 CC renal carcinoma, fibrosarcoma, rhabdosarcoma cell or a pancreatic cancer.  
 CC The present sequence is used in the exemplification of the present  
 CC invention.  
 XX Sequence 878 AA;  
 SQ

Query Match 56.6%; Score 1271.5; DB 8; Length 878;  
 Best Local Similarity 63.8%; Pred. No. 2.1e-75;  
 Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;  
 QY 2 DKTHTCPCPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDSHEDPEVKFNWYD 61  
 DB 1 DKTHTCPCPAPLLGGPSVFLPPPKKDTLMISRTPEVTCVVVDSHEDPEVKFNWYD 60  
 QY 62 GVEVHNKTPREEQYNSTRVSVLTVLHODWLNGKEYCKVSKNKPAPTEKTSKAK 121  
 DB 61 GVEVHNKTPREEQYNSTRVSVLTVLHODWLNGKEYCKVSKNKPAPTEKTSKAK 120

QY 122 GQPREQVYTLPPSRDELTKQVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLD 181  
 DB 121 GQPREQVYTLPPSRDELTKQVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLD 180  
 QY 182 DGSFFLYSKLTVDKSRWQGNVFSVMHEALHNHYTQKSLSLSPGK-----ETFPKP 234  
 DB 181 DGSFFLYSKLTVDKSRWQGNVFSVMHEALHNHYTQKSLSLSPGKGGGGGGGFFE- 239  
 QY 235 YLHYDEE---TSHQLLCKDKPPGTYLKQH-----CTAKWK-----TVC 269  
 DB 240 ----DSEPISSH-----GNVTQVYFVGHKPGRNTTORHRLDIQIMIMNGTLY 286  
 QY 270 APCPDHYIT---DSWHTSDECLYCSPVCKELQVYVQECNRTHNRVCECK-EGRYLE---- 321  
 DB 287 IAARDHIYTVDTIDTSHTEB--IYCS---KKLTWKSQAD-----VDTCRMKGKHKDECHN 336  
 QY 322 -IEFCLKHSRCPGFGVQAGTPERNVCKRC-----PDGPFNSNETSSKAPC---RKHT 371  
 DB 337 FIKVLLKND----DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCPCYAKHA 389  
 QY 372 NCSVF 376  
 DB 390 NVALF 394  
 RESULT 9  
 ADO40298  
 ID ADO40298 standard; protein; 878 AA.  
 AC ADO40298;  
 XX 15-JUL-2004 (first entry)  
 DT Human semaphorin-like protein NOV2u.  
 DE Human; semaphorin; NOV2; angiogenesis inhibitor; gene therapy;  
 KW cell migration; angiogenesis; actin filament formation;  
 KW angiogenic-related disorder; loss of balance; weight loss; slow speech;  
 KW jaundice; fatigue; pain; blood in urine; anaemia; swollen bone; cancer;  
 KW pancreatic cancer; renal cancer; neuroblastoma; wound healing;  
 KW tissue regeneration.  
 XX Homo sapiens.  
 OS US2004018977-A1.  
 PN 29-JAN-2004.  
 PD 30-MAY-2003; 2003US-00449548.  
 XX 09-MAR-1999; 99US-0123667P.  
 PR 08-MAR-2000; 2000US-00520781.  
 PR 09-APR-2002; 2002US-0371002P.  
 PR 30-MAY-2002; 2002US-0384798P.  
 PR 09-AUG-2002; 2002US-0402407P.  
 PR 28-JAN-2003; 2003US-0443062P.  
 PR 31-MAR-2003; 2003US-00403676.  
 XX (ALVA/) ALVAREZ E.  
 PA (ANDE/) ANDERSON D W.  
 PA (DHAN/) DHANABAL M.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (LARO/) LAROCHELLE W J.  
 PA (LICH/) LICHENSTEIN H S.  
 PA (LILL/) LI L.  
 PA (OOIC/) OOI C E.  
 PA (PADI/) PADIGARU M.  
 PA (SHIM/) SHIMKETS R A.  
 PA (ZHON/) ZHONG M.  
 XX Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochele WJ;  
 PI Lichenstein HS, Li L, Ooi CE, Padigar M, Shimkets RA, Zhong M;



```
SQ Sequence 409 AA;
Query Match 55.9%; Score 1254.5; DB 7; Length 409;
Best Local Similarity 62.3%; Pred. No. 1.1e-74;
Matches 256; Conservative 27; Mismatches 71; Indels 57; Gaps 7;

QY 1 MDKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 16 LDKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 75

QY 61 DGVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETKISKAK 120
DB 76 DGVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETKISKAK 135

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 136 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 195

QY 181 SDGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPKETTTPPKYLHYDE 240
DB 196 SDGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPKETTTPPKYLHYDE 255

QY 241 -ETSHQLLCKDKCPP-GTYLKHCHTAKWTKVCAPCPDHYTDSWHTSDECLYCSPVCKELQ 298
DB 256 PEPEGSLOGDONQIAAHVISEASSTTSVLQWAEKGYTMS----- 297

QY 299 YVQECNRTHNRVCECKEGR-----YLEIEFCLKHRSCTPPGFGVQAGTPERN 346
DB 298 -----NNLVLENGKQLTVKRQGLYIYAQVTFCSNREA-----SSQAPFFIA 339

QY 347 TVCKRCPDGF-----FSNETSKACPKRHTNCSVGLLLLTQKGNATHDNI 391
DB 340 SLCKSPGRFERILLRAANTHSSAKPCGQO-SIHGGVPELOPGASVFVNV 389

RESULT 11
AAM52156
ID AAM52156 standard; protein; 731 AA.
XX
AC AAM52156;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMF-G-1 heavy chain/DNase I fusion protein 1.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB001324.
XX
PR 03-APR-2000; 2000GB-00008049.
XX
PR 02-OCT-2000; 2000US-0237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
WPI; 2001-662969/76.
XX
DR Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity.
XX
PS Claim 20; Fig 7; 176pp; English.
XX
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CC The invention relates to a compound which comprises a target cell-
CC specific portion, comprising an humanised monoclonal antibody, having
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
CC fragment and a cytotoxic portion having endonucleolytic activity.
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis
XX
SQ Sequence 731 AA;

Query Match 55.6%; Score 1249; DB 4; Length 731;
Best Local Similarity 65.6%; Pred. No. 5.2e-74;
Matches 254; Conservative 15; Mismatches 56; Indels 62; Gaps 6;

QY 2 DKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 241 DKTHCTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300

QY 62 DGVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETKISKAK 121
DB 301 DGVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDLNKGKEYCKVSNKALPAPIETKISKAK 360

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420

QY 182 DGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPKETTTPPKYLHYDE 241
DB 421 DGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPKETTTPPKYLHYDE 480

QY 242 TSHQLLCKDKCPGTYLQK-----HCTAKWK---TVCAFCPDHYV----- 277
DB 481 TFGETKMSNATLVSVIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQADPTDTHYVWSE 540

QY 278 -----TDSWHTSDECLYCSPVCKELQYVQECNRTHNRVCECK 315
DB 541 PLGRNSYKERYLFVYRPPDOVSADVSYDDGCEPCG-----NDTFNREPAIV 587

QY 316 E--GRAYLEI-EFCLKHRSCTPPGFGVQ 339
DB 588 RFFSRFTVEVREPAIVPLHAAPGDAVAE 614

RESULT 12
AAM52159
ID AAM52159 standard; protein; 741 AA.
XX
AC AAM52159;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMF-G-1 heavy chain/DNase I fusion protein 4.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB001324.
XX
PR 03-APR-2000; 2000GB-00008049.
PR 02-OCT-2000; 2000US-0237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
WPI; 2001-662969/76.
XX
DR
```

XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanized monoclonal antibody having specificity for  
FT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity.  
XX  
PS Claim 20; Fig 10; 176pp; English.  
XX  
CC The invention relates to a compound which comprises a target cell-  
CC specific portion, comprising an humanised monoclonal antibody, having  
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding  
CC fragment and a cytotoxic portion having endonucleolytic activity, the  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis  
XX  
SQ Sequence 741 AA;

Query Match 55.6%; Score 1249; DB 4; Length 741;  
Best Local Similarity 65.6%; Pred. No. 5.3e-74;  
Matches 254; Conservative 15; Mismatches 56; Indels 62; Gaps 6;  
QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENNYVD 61  
Db 241 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYYD 300  
QY 62 GVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
Db 301 GVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360  
QY 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181  
Db 361 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420  
QY 182 DGSFFLYSKLTVDKSRWQGNFSCSMHEALHNYHTQKLSLSLSPCKETFPKYLHYDEE 241  
Db 421 DGSFFLYSKLTVDKSRWQGNFSCSMHEALHNYHTQKLSLSLSPCKETFPKYLHYDEE 480  
QY 242 TSHQLLCKDCPPGTLYLKQ-----HCTAKWK---TVCAPCPDHY----- 277  
Db 481 TFGETKMSNATLVSYIVQILSRDYIALVQEVDRDHLTAVGKLLDNLNQADPTVHYVWSE 540  
QY 278 -----TDSWHTSDECLYCSPVCKELQYVVKQECNRTNHRVCECK 315  
Db 541 PLGRNYSKERYLFVYRPDQVSAVDSYVYDDGCEPCG-----NDTFNREPAIV 587  
QY 316 E--GRYLEI-EFCLKHSRCPGFGVQ 339  
Db 588 RPFSTRTEVREFAIVPLHAAPGDAVAE 614

RESULT 13  
ADP75168  
ID ADP75168 standard; protein; 412 AA.  
XX  
AC ADP75168;  
XX  
DT 12-AUG-2004 (first entry)  
DE Fusion construct psl181 Fc:TNFalpha protein.  
XX  
KW fusion protein; immunoglobulin; Fc region; TNF; tumour necrosis factor;  
KW Fast; TNF-alpha; TNF-gamma; TRAIL; ED1; ED2; ED3; ED4; ED5; ED6; ED7;  
KW depilatory; gene therapy; cellular therapy; ectodermal dysplasia;  
KW x-linked immune deficiency; hyper IgM; alopecia; hirsutism; sweat gland;  
KW sebaceous gland.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..15  
FT /note= "HA signal"

FT Region 18. .243  
FT /note= "hlg Fc aa248-473 of gi2765420"  
FT Peptide 246. .259  
FT /note= "linker peptide"  
FT Region 264. .412  
FT /note= "hTNFalpha aa80-228"  
XX  
PN DE10205583-A1.  
XX  
PD 21-AUG-2003.  
XX  
PF 11-FEB-2002; 2002DE-01005583.  
XX  
PR 10-FEB-2002; 2002DE-01005368.  
XX  
PA (APOX-) APOXIS SA.  
XX  
PI Gaide O, Schneider P, Tschopp J;  
XX WPI; 2003-647319/62.  
DR N-PSDB; ADP75167.  
XX  
PT New recombinant fusion protein, useful for treating deficiency of tumor  
PT necrosis factor ligand, particularly ectodermal dysplasia, comprises the  
PT ligand and immunoglobulin fragment.  
XX  
PS Claim 8; Fig F; 22pp; German.  
XX  
CC This invention describes a novel recombinant fusion protein which  
CC comprises an immunoglobulin Fc segment, the extracellular region of a  
CC tumour necrosis factor (TNF) and optionally a transition region,  
CC including a linker. The TNF ligands used in the method include FasL, TNF-  
CC alpha or TNF-gamma, TRAIL or most preferred, ED1 or 2. The Fc fragment  
CC contains the hinge region and domains CH2 and CH3 of the Fc segment of an  
CC IgG, particularly human. The linker optionally includes a protease  
CC cleavage site. The N-terminus of construct may have a signal sequence,  
CC secretory signal sequence and/or tag (e.g. Flag or His). The products of  
CC the invention have dermatological and depilatory activity. The construct,  
CC or other therapeutic agents, are administered parenterally (especially  
CC intravenously or intra-arterially) during pregnancy, especially as early  
CC as possible, e.g. for humans, in the first 3 months, every second day for  
CC at least 14 days. Nucleic acid encoding the construct, related vectors  
CC and transfected host cells, are useful in gene/cellular therapy of  
CC genetic disorders associated with defective expression of TNF ligand,  
CC particularly ectodermal dysplasia (specifically the X-linked hypohydrotic  
CC form or X-linked immune deficiency with hyper IgM) and also alopecia,  
CC hirsutism and inadequate functioning of the sweat and sebaceous glands.  
CC The fusion protein construct is soluble but still retains ability to  
CC mimic the physiological effects of TNF ligand. This sequence represents  
CC the fusion construct Fc-TNFalpha.  
XX  
SQ Sequence 412 AA;

Query Match 55.4%; Score 1244; DB 7; Length 412;  
Best Local Similarity 64.3%; Pred. No. 5.7e-74;  
Matches 252; Conservative 22; Mismatches 50; Indels 68; Gaps 7;  
QY 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYY 60  
Db 16 LDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNYY 75  
QY 61 DGEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120  
Db 76 DGEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 135  
QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180  
Db 136 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 195  
QY 181 SDGSFFLYSKLTVDKSRWQGNFSCSMHEALHNYHTQKLSLSLSPCKETFPFK----- 234  
Db 196 SDGSFFLYSKLTVDKSRWQGNFSCSMHEALHNYHTQKLSLSLSPCKETFPFK----- 255

QY 235 -----YLHYDEETSHQLLCKCPGTYLKQCHTAKWKVCAPCPDHYTDSWHTSDECLY 289  
Db 256 PEPESLQSDKPVAAH-----VV 272  
QY 290 CSPVCK-ELQYVQECNR-----THNRVCECKEGRYL-EIEFCLKHRSCPPGFGWQ 339  
Db 273 ANPAESQLQWLNRRANALLANGVELRDNLQVVPSEGLYLYSOVLFKGGC-PSTHVL 331  
QY 340 AGTPERTVCKRCPDGGFFSNETSCKAPCRKHT 371  
Db 332 THTISRAVSQTKVNLSS---AIKSPCQRET 360

RESULT 14  
ADC98610  
ID ADC98610 standard; protein; 489 AA.  
XX AC ADC98610;  
XX DT 01-JAN-2004 (first entry)  
XX DE Human angiogenesis related secreted protein NOV1u SEQ ID NO:44.  
XX KW human; angiorestin; secreted protein; angiogenesis;  
KW fibrinogen binding domain; coiled coil domain; cytosolic;  
KW antiangiogenic; cardiant; vasotrophic; vulnary; osteopathic;  
KW antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
KW gene therapy; angiogenesis inhibitor; tumour; tumour metastasis;  
KW ischaemic heart disease; peripheral vascular disease; wound healing;  
KW bone repair; rheumatoid arthritis; diabetic retinopathy.  
XX OS Homo sapiens.  
XX PN WO2003078648-A2.  
XX PD 25-SEP-2003.  
XX PF 11-MAR-2003; 2003WO-US007586.  
XX PR 11-MAR-2002; 2002US-0363266P.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Dhanabal M, Wu F, Larochele WJ, Lichenstein HS;  
XX DR WPI; 2003-748655/70.  
XX DR N-PSDB; ADC98609.  
XX PT New isolated Angiorestin polynucleotide and polypeptides, useful for  
PT inhibiting the growth of a tumor, tumor metastasis or angiogenesis, and  
PT for treating ischemic heart disease, rheumatoid arthritis and diabetic  
PT retinopathy.  
XX PS Claim 3; SEQ ID NO 44; 88pp; English.  
XX CC The present invention describes human angiorestin secreted proteins  
CC having antiangiogenesis activity. More specifically described is an  
CC isolated polynucleotide (I) encoding a fibrinogen binding domain (FBD)  
CC and a coiled coil (CC) domain. (I) has cytostatic, antiangiogenic,  
CC cardiant, vasotrophic, vulnary, osteopathic, antirheumatic, and can be  
CC antiarthritic, antidiabetic and ophthalmological activities, and can be  
CC used in gene therapy, and as an angiogenesis inhibitor. Methods and  
CC compositions of the present invention of inhibiting angiorestin  
CC proteins, are useful for inhibiting the growth of a tumour, tumour  
CC metastasis and/or angiogenesis, and including disorders such as ischaemic  
CC heart disease, peripheral vascular disease, wound healing, bone repair,  
CC rheumatoid arthritis and diabetic retinopathy. The present sequence is  
CC used in the exemplification of the present invention.  
XX SQ Sequence 489 AA;

Query Match 55.3%; Score 1241; DB 7; Length 489;  
Best Local Similarity 85.5%; Pred. No. 1.1e-73;

Matches 236; Conservative 4; Mismatch 14; Indels 22; Gaps 2;  
QY 2 DKHTCTCPCPABELLGGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Db 1 DKHTCTCPCPABELLGGPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60  
QY 62 GVEVHNATKPREEOVNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKAK 121  
Db 61 GVEVHNATKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKAK 120  
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181  
Db 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 180  
QY 182 DGSFPLYSKLTVDKSRWQQGNVSCVMHEALHNYHTQKSLSPGKGGGGGGGIBQIRD 240  
Db 181 DGSFPLYSKLTVDKSRWQQGNVSCVMHEALHNYHTQKSLSPGKGGGGGGGIBQIRD 240  
QY 229 -----ETPEPKYLVHDEETSHQLLCKCPGTYLKQ 259  
Db 241 PGYPRDLMPDP-----DLATSPKSPFKIPPTFINE 272

RESULT 15  
AAB17951  
ID AAB17951 standard; protein; 248 AA.  
XX AC AAB17951;  
XX DT 31-OCT-2000 (first entry)  
XX DE Fc-TNF-alpha inhibitor fusion protein sequence SEQ ID NO:1056.  
XX KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;  
KW thrombosis; pharmaceutical.  
XX OS Synthetic.  
XX PN WO2000024782-A2.  
XX PD 04-MAY-2000.  
XX PF 25-OCT-1999; 99WO-US025044.  
XX PR 23-OCT-1998; 98US-0105371P.  
XX PR 22-OCT-1999; 99US-00428082.  
XX PA (AMGE-) AMGEN INC.  
XX PI Feige U, Liu C, Cheatham J, Boone TC;  
XX WPI; 2000-350702/30.  
XX DR N-PSDB; AAA69501.  
XX PT Novel composition of matter comprising an Fc domain and pharmacologically  
XX active peptides, useful for treating cancer and autoimmune diseases.  
XX PS Example 4; Page 568-569; 608pp; English.  
XX CC The present invention describes composition of matter (I) comprising an  
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-  
CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P3-(L4)f-P4 where P1, P2,  
CC P3, and P4 = are each independently sequences of pharmacologically active  
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,  
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1  
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,

CC thrombolytic and immunosuppressive activities. DNAs, vectors and host  
CC cells from the present invention can be used for producing pharmaceutical  
CC compositions. The compositions are useful for treating cancer, asthma,  
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than  
CC a Fab domain) can provide a longer half-life or incorporate functions  
CC such as Fc receptor binding, protein A binding, complement fixation, and  
CC possibly placental transfer. AAG69443 to AAG69526 and AAB16955 to  
CC AAB18003 represent nucleotide and amino acid sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 248 AA;

Query Match 55.2%; Score 1240; DB 3; Length 248;  
Best Local Similarity 95.1%; Pred. No. 5.7e-74;  
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
Db 1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
Qy 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120  
Db 61 DGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120  
Qy 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180  
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180  
Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGKTFPPKYLHYDE 240  
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGKGGGGDLPHYK 240  
Qy 241 ETS 243  
Db 241 NTS 243

Search completed: March 8, 2005, 14:38:22  
Job time : 87.1064 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:28:42 ; Search time 21.9235 Seconds  
(without alignments)  
1365.399 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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3: /cgn2\_6/prodata/1/iaa/6A COMB.pep:\*

4: /cgn2\_6/prodata/1/iaa/6B COMB.pep:\*

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6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1240	55.2	248	4	US-09-428-082B-1056
2	1238	55.1	228	4	US-09-428-082B-2
3	1238	55.1	228	4	US-09-847-249A-2
4	1238	55.1	228	4	US-09-840-669B-2
5	1238	55.1	228	4	US-09-843-221A-2
6	1238	55.1	228	4	US-09-709-704A-2
7	1238	55.1	228	4	US-09-422-838C-5
8	1238	55.1	243	4	US-09-428-082B-1068
9	1238	55.1	247	4	US-09-428-082B-6
10	1238	55.1	248	4	US-09-428-082B-1060
11	1238	55.1	252	4	US-09-428-082B-1064
12	1238	55.1	253	4	US-09-428-082B-16
13	1238	55.1	268	4	US-09-428-082B-8
14	1238	55.1	269	4	US-09-422-838C-46
15	1238	55.1	277	4	US-09-428-082B-22
16	1237	55.1	389	3	US-09-131-247-14
17	1237	55.1	389	4	US-09-784-623-14
18	1234	54.9	229	4	US-09-122-144-2
19	1234	54.9	347	1	US-07-940-861-43
20	1234	54.9	347	1	US-08-459-512-43
21	1234	54.9	347	2	US-08-459-657-43
22	1234	54.9	347	2	US-08-460-132-43
23	1234	54.9	347	3	US-08-466-465-8
24	1234	54.9	347	4	US-09-730-465-8
25	1234	54.9	347	5	PCT-US92-02050-43
26	1234	54.9	399	4	US-09-832-659A-2
27	1234	54.9	418	4	US-09-832-659A-42

28	1234	54.9	423	4	US-09-832-659A-44	Sequence 44, Appl
29	1234	54.9	446	4	US-09-157-452B-12	Sequence 12, Appl
30	1234	54.9	482	3	US-09-189-129-2	Sequence 2, Appl
31	1234	54.9	482	4	US-09-824-286-2	Sequence 2, Appl
32	1233.5	54.9	394	4	US-09-854-864-31	Sequence 31, Appl
33	1233	54.9	232	2	US-08-595-043A-50	Sequence 50, Appl
34	1233	54.9	232	4	US-09-968-362A-26	Sequence 26, Appl
35	1233	54.9	235	3	US-09-131-247-6	Sequence 6, Appl
36	1233	54.9	235	4	US-09-784-623-6	Sequence 12, Appl
37	1233	54.9	247	4	US-09-428-082B-12	Sequence 1058, Ap
38	1233	54.9	248	4	US-09-428-082B-1058	Sequence 1062, Ap
39	1233	54.9	250	4	US-09-428-082B-1070	Sequence 1070, Ap
40	1233	54.9	252	4	US-09-428-082B-1066	Sequence 1066, Ap
41	1233	54.9	253	4	US-09-428-082B-18	Sequence 18, Appl
42	1233	54.9	269	4	US-09-428-082B-10	Sequence 10, Appl
43	1233	54.9	277	4	US-09-428-082B-20	Sequence 20, Appl
44	1233	54.9	281	4	US-09-854-864-10	Sequence 10, Appl
45	1233	54.9				

ALIGNMENTS

RESULT 1

US-09-428-082B-1056  
; Sequence 1056, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1056  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS  
US-09-428-082B-1056

Query Match 55.2%; Score 1240; DB 4; Length 248;  
Best Local Similarity 95.1%; Pred. No. 2.2e-98;  
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy	1	MDKTHCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60
Db	1	MDKTHCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60
Qy	61	DGVEVHNATKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKA	120
Db	61	DGVEVHNATKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKA	120
Qy	121	KQOPREPQYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	180
Db	121	KQOPREPQYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	180
Qy	181	SDGSFLLYSKLTVDKSRWQQGNVFCSVNHEALHHYTKOISLSLSPGKTFPPKYLHYDE	240
Db	181	SDGSFLLYSKLTVDKSRWQQGNVFCSVNHEALHHYTKOISLSLSPGKTFPPKYLHYDE	240
Qy	241	ETS 243	
Db	241	NTS 243	

RESULT 2  
US-09-428-082B-2  
; Sequence 2, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-428-082B-2

Query Match 55.1%; Score 1238; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.9e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
DB 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120  
DB 61 DGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120  
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 3  
US-09-847-249A-2  
; Sequence 2, Application US/09847249A  
; Patent No. 6677136  
; GENERAL INFORMATION:  
; APPLICANT: MARSHALL, WILLIAM S.  
; APPLICANT: STARK, KEVIN LEE  
; TITLE OF INVENTION: GLUCAGON ANTAGONIST  
; FILE REFERENCE: A-693  
; CURRENT APPLICATION NUMBER: US/09/847,249A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,436  
; PRIOR FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-249A-2

Query Match 55.1%; Score 1238; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.9e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
DB 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120  
DB 61 DGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120  
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 4  
US-09-840-669B-2  
; Sequence 2, Application US/09840669B  
; Patent No. 6743778  
; GENERAL INFORMATION:  
; APPLICANT: KOHNO, TADAHIKO  
; TITLE OF INVENTION: APO-AI/AII PEPTIDE DERIVATIVES  
; FILE REFERENCE: A-690  
; CURRENT APPLICATION NUMBER: US/09/840,669B  
; CURRENT FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: 60/198,920  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-840-669B-2

Query Match 55.1%; Score 1238; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 2.9e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
DB 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120  
DB 61 DGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120  
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 5  
US-09-843-221A-2  
; Sequence 2, Application US/09843221A  
; Patent No. 6756480  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENIUK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27

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; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-2

Query Match          55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
DB 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 6
US-09-709-704A-2
; Sequence 2, Application US/09709704A
; Patent No. 6808902
; GENERAL INFORMATION:
; APPLICANT: TREUHEIT, MICHAEL J.
; APPLICANT: O'CONNER, SHEILA R.
; APPLICANT: KOSKY, ANDREW A.
; TITLE OF INVENTION: PROCESS FOR CORRECTION OF A DISULFIDE MISFOLD IN FC MOLECULES
; FILE REFERENCE: A-584
; CURRENT APPLICATION NUMBER: US/09/709,704A
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,188
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-704A-2

Query Match          55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
DB 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 7
US-09-709-704A-2
; Sequence 2, Application US/09709704A
; Patent No. 6808902
; GENERAL INFORMATION:
; APPLICANT: TREUHEIT, MICHAEL J.
; APPLICANT: O'CONNER, SHEILA R.
; APPLICANT: KOSKY, ANDREW A.
; TITLE OF INVENTION: PROCESS FOR CORRECTION OF A DISULFIDE MISFOLD IN FC MOLECULES
; FILE REFERENCE: A-584
; CURRENT APPLICATION NUMBER: US/09/709,704A
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,188
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-704A-2

Query Match          55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
DB 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 8
US-09-428-082B-1068
; Sequence 1068, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1068
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC MMP INHIBITOR
US-09-428-082B-1068

Query Match          55.1%; Score 1238; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.2e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-422-838C-5
; Sequence 5, Application US/09422838C
; Patent No. 6835809
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: Thrombopoietic Compounds
; FILE REFERENCE: 01017/36283
; CURRENT APPLICATION NUMBER: US/09/422,838C
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,348
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-422-838C-5

Query Match          55.1%; Score 1238; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.9e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
DB 61 DQVEVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEGSSNQPNNTKTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 8
US-09-428-082B-1068
; Sequence 1068, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1068
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC MMP INHIBITOR
US-09-428-082B-1068

Query Match          55.1%; Score 1238; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 3.2e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
Db 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228  
Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

## RESULT 9

US-09-428-082B-6  
; Sequence 6, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc-TMP  
US-09-428-082B-6

Query Match 55.1%; Score 1238; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 3.3e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
Db 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228  
Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

## RESULT 10

US-09-428-082B-1060  
; Sequence 1060, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1060  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: FC-IL-1 ANTAGONIST  
US-09-428-082B-1060

Query Match 55.1%; Score 1238; DB 4; Length 248;  
Best Local Similarity 100.0%; Pred. No. 3.3e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
Db 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
Db 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228  
Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

## RESULT 11

US-09-428-082B-1064  
; Sequence 1064, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1064  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc-VEGF ANTAGONIST  
US-09-428-082B-1064

Query Match 55.1%; Score 1238; DB 4; Length 252;  
Best Local Similarity 100.0%; Pred. No. 3.3e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
Db 1 MDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

## RESULT 12

US-09-428-082B-16  
; Sequence 16, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428, 082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 16  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc-BMP  
US-09-428-082B-16

Query Match 55.1%; Score 1238; DB 4; Length 253;  
Best Local Similarity 100.0%; Pred. No. 3.4e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120  
DB 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120  
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

## RESULT 13

US-09-428-082B-8  
; Sequence 8, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428, 082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 8

; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc-TMP-TMP  
US-09-428-082B-8

Query Match 55.1%; Score 1238; DB 4; Length 268;  
Best Local Similarity 100.0%; Pred. No. 3.6e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120  
DB 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120  
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

## RESULT 14

US-09-422-838C-46  
; Sequence 46, Application US/09422838C  
; Patent No. 6835809  
; GENERAL INFORMATION:  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: CHEETHAM, JANET C.  
; TITLE OF INVENTION: Thrombopoietic Compounds  
; FILE REFERENCE: 01017/36263  
; CURRENT APPLICATION NUMBER: US/09/422,838C  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,348  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-422-838C-46

Query Match 55.1%; Score 1238; DB 4; Length 269;  
Best Local Similarity 100.0%; Pred. No. 3.7e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
QY 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120  
DB 61 DGVEVHNATKPREEQYNSTYRVSVLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 120  
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

## RESULT 15

US-09-428-082B-22  
; Sequence 22, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc-EMP-EMP  
US-09-428-082B-22

Query Match 55.1%; Score 1238; DB 4; Length 277;  
Best Local Similarity 100.0%; Pred. No. 3.8e-98;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60  
  
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120  
  
QY 121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 KGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSMVEALHNHYTOKSLSLSPGK 228  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 SDGSFFLYSKLTVDKSRWQQGNVFCSMVEALHNHYTOKSLSLSPGK 228

Search completed: March 8, 2005, 14:48:15  
Job time : 22.9235 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:44:50 ; Search time 60.5885 Seconds  
(without alignments)  
2177.757 Million cell updates/sec

Title: US-09-389-782a-8  
Perfect score: 2246  
Sequence: 1 MDKTHCPCPAPPELLGGPS.....QKGNATHDNCISGSESTOK 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2246	100.0	401	10	US-09-389-782-8
2	1271.5	56.6	861	15	US-10-449-548-52
3	1271.5	56.6	861	15	US-10-403-676-52
4	1271.5	56.6	878	15	US-10-449-548-54
5	1271.5	56.6	878	15	US-10-403-676-54
6	1249	55.6	731	9	US-09-825-012-46
7	1249	55.6	741	9	US-09-825-012-55
8	1241	55.3	489	15	US-10-385-802-44
9	1240	55.2	248	15	US-10-609-217-1056
10	1240	55.2	248	15	US-10-632-388-1056
11	1240	55.2	248	15	US-10-651-723-1056
12	1240	55.2	248	15	US-10-645-761-1056
13	1240	55.2	248	15	US-10-666-696-1056

14	1240	55.2	248	15	US-10-653-048-1056
15	1238	55.1	228	9	US-09-847-712-2
16	1238	55.1	228	9	US-09-847-277-2
17	1238	55.1	228	10	US-09-847-249A-2
18	1238	55.1	228	10	US-09-843-221A-2
19	1238	55.1	228	10	US-09-840-669B-2
20	1238	55.1	228	14	US-10-269-806-32
21	1238	55.1	228	14	US-10-145-206-2
22	1238	55.1	228	15	US-10-609-217-2
23	1238	55.1	228	15	US-10-632-388-2
24	1238	55.1	228	15	US-10-651-723-2
25	1238	55.1	228	15	US-10-645-761-2
26	1238	55.1	228	15	US-10-666-696-2
27	1238	55.1	228	15	US-10-653-048-2
28	1238	55.1	228	16	US-10-666-480-60
29	1238	55.1	228	17	US-10-925-183-2
30	1238	55.1	243	14	US-10-269-806-152
31	1238	55.1	243	15	US-10-609-217-1068
32	1238	55.1	243	15	US-10-632-388-1068
33	1238	55.1	243	15	US-10-651-723-1068
34	1238	55.1	243	15	US-10-645-761-1068
35	1238	55.1	243	15	US-10-666-696-1068
36	1238	55.1	243	15	US-10-653-048-1068
37	1238	55.1	247	15	US-10-609-217-6
38	1238	55.1	247	15	US-10-632-388-6
39	1238	55.1	247	15	US-10-651-723-6
40	1238	55.1	247	15	US-10-645-761-6
41	1238	55.1	247	15	US-10-666-696-6
42	1238	55.1	247	15	US-10-653-048-6
43	1238	55.1	248	15	US-10-609-217-1060
44	1238	55.1	248	15	US-10-632-388-1060
45	1238	55.1	248	15	US-10-651-723-1060

ALIGNMENTS

RESULT 1  
US-09-389-782-8  
; Sequence 8, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-8

Query Match 100.0%; Score 2246; DB 10; Length 401;  
Best Local Similarity 100.0%; Pred. No. 3.4e-145;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60
DB	1	MDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	60
QY	61	DGVEVHNATKREQYNSYTYVSVLTVLHQDLNGLKEYCKVSNKALPAPIEKTISKA	120
DB	61	DGVEVHNATKREQYNSYTYVSVLTVLHQDLNGLKEYCKVSNKALPAPIEKTISKA	120
QY	121	KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	180
DB	121	KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	180

QY 191 SDGFFLYSKLTVDKSRWQGNVSCSVMHSEALHNHYTKSLSPKGTFFPKYLHYDE 240  
DB 181 SDGFFLYSKLTVDKSRWQGNVSCSVMHSEALHNHYTKSLSPKGTFFPKYLHYDE 240  
QY 241 ETSHQLLCDKCPGGYLLKQHTAKWTVCAPCPDHYTDSWHTSDECLYSPVKELQYV 300  
DB 241 ETSHQLLCDKCPGGYLLKQHTAKWTVCAPCPDHYTDSWHTSDECLYSPVKELQYV 300  
QY 301 KOENRTHNRVCECKEGRYLEIEFCLKHSRCPGGVGVQAGTPERNTVCKRCPDGPFSNE 360  
DB 301 KOENRTHNRVCECKEGRYLEIEFCLKHSRCPGGVGVQAGTPERNTVCKRCPDGPFSNE 360  
QY 361 TSSKAPCKRHTNCSVFGLLLTQKNATHDNCNSSESTQK 401  
DB 361 TSSKAPCKRHTNCSVFGLLLTQKNATHDNCNSSESTQK 401

## RESULT 2

US-10-449-548-52  
; Sequence 52, Application US/10449548  
; Publication No. US20040018977A1  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Enrique  
; APPLICANT: Anderson, David W.  
; APPLICANT: Dhanabal, Mohanraj  
; APPLICANT: Khramcov, Nikolai V.  
; APPLICANT: LaRoche, William J.  
; APPLICANT: Li, Li  
; APPLICANT: Lichenstein, Henri  
; APPLICANT: Ooi, Chean Eng  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME  
; FILE REFERENCE: 15966-540CIP2  
; CURRENT APPLICATION NUMBER: US/10/449,548  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: 09/520,781  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/123,667  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 60/234,082  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 60/233,798  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 60/174,485  
; PRIOR FILING DATE: 2000-01-04  
; PRIOR APPLICATION NUMBER: 10/403,676  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: 60/371,002  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/384,798  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/402,407  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 60/443,062  
; PRIOR FILING DATE: 2003-01-28  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 52  
; LENGTH: 861  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-449-548-52

Query Match 56.6%; Score 1271.5; DB 15; Length 861;  
Best Local Similarity 63.8%; Pred. No. 2.4e-78;  
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;  
QY 2 DKHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
DB 1 DKHTCCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNATKPREOVNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAK 121  
DB 61 GVEVHNATKPREOVNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAK 120  
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181  
DB 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 182 DGSFFLYSKLTVDKSRWQGNVSCSVMHSEALHNHYTKSLSPKGTFFPKYLHYDE 234  
DB 181 DGSFFLYSKLTVDKSRWQGNVSCSVMHSEALHNHYTKSLSPKGTFFPKYLHYDE 239  
QY 235 YLHYDEE---TSHQLLCKDCPBGTYLKOH-----CTAKWK-----TVC 269  
DB 240 ---DSEPIISISH-----GNTKQYFVFGVGHKPGRNTTQHRHLDIQIMINWGTLY 286  
QY 270 APCPDHYT---DSWHTSDECLYSPVKELQYVQAGTPERNTVCKRCPDGPFSNE 321  
DB 287 TAARDHIYTVDTIDTSHTEE---IYCS---KLTWKSROAD---VDTCRMKGKHKDECHN 336  
QY 322 -IEFCLKHSRCPGGVGVQAGTPERNTVCKRCPDGPFSNETSSKAPC---RKHT 371  
DB 337 FIKVLLKND---DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCPYDAKHA 389  
QY 372 NCSVF 376  
DB 390 NVALF 394

## RESULT 3

US-10-403-676-52  
; Sequence 52, Application US/10403676  
; Publication No. US20040029150A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook II, John  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Groesse, William M.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: LaRoche, William J.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Li, Li  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Reiger, Daniel  
; APPLICANT: Rothenberg, Mark E.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Stone, David J.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zerhusen, Bryan D.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-573B  
; CURRENT APPLICATION NUMBER: US/10/403,676  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: 60/123,667  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 09/520,781  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 09/957,187  
; PRIOR FILING DATE: 2001-09-19

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; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 52
; LENGTH: 861
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-52

Query Match          56.6%; Score 1271.5; DB 15; Length 861;
Best Local Similarity 63.8%; Pred. No. 2.4e-78;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKHTCCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 1 DKHTCCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 61 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

QY 182 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK-----ETFPKP 234
DB 181 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGKGGGGGGGFP 239

QY 235 YLHYDEE---TSHQLLCKDCPPGTYLKQH-----CTAKWK-----TVC 269
DB 240 ----DSEPTISISH-----GNVTKQYPVFVGHKPGRNTTQHRHLDIQIMINMGTY 286

QY 270 APCPDHYIT---DSWHTSDECLYCSVPCKELQVYKQECNRTNRYCECK-EGRYLE- 321
DB 287 IAARDHIYTVDTIDTSHTEE--IYCS---KKLTWKSROAD-----VDTCRMKGKHKDECHN 336

QY 322 -IEFCLKHSRCPGFGVQAGTPERNVTCKRC-----PDGFFSNETSSKAPC---RKHT 371
DB 337 FIKVLLKKND----DALFVCGTNAFPNFCRNYKMDTLEP---FGDEFSGMARCPCYDAKHA 389

QY 372 NCSVP 376
DB 390 NVALF 394

RESULT 4
US-10-449-548-54
; Sequence 54, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRoche, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
```

```
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 54
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-548-54
```

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Query Match          56.6%; Score 1271.5; DB 15; Length 878;
Best Local Similarity 63.8%; Pred. No. 2.4e-78;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY 2 DKHTCCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 1 DKHTCCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 60

QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 61 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

QY 182 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK-----ETFPKP 234
DB 181 DGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGKGGGGGGGFP 239

QY 235 YLHYDEE---TSHQLLCKDCPPGTYLKQH-----CTAKWK-----TVC 269
DB 240 ----DSEPTISISH-----GNVTKQYPVFVGHKPGRNTTQHRHLDIQIMINMGTY 286

QY 270 APCPDHYIT---DSWHTSDECLYCSVPCKELQVYKQECNRTNRYCECK-EGRYLE- 321
DB 287 IAARDHIYTVDTIDTSHTEE--IYCS---KKLTWKSROAD-----VDTCRMKGKHKDECHN 336

QY 322 -IEFCLKHSRCPGFGVQAGTPERNVTCKRC-----PDGFFSNETSSKAPC---RKHT 371
DB 337 FIKVLLKKND----DALFVCGTNAFPNFCRNYKMDTLEP---FGDEFSGMARCPCYDAKHA 389

QY 372 NCSVP 376
DB 390 NVALF 394

RESULT 5
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US-10-403-676-54
; Sequence 54, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRoche, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/423,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 54
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-54

Query Match      56.6%; Score 1271.5; DB 15; Length 878;
Best Local Similarity 63.8%; Pred. No. 2.4e-78;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY      2 DKHTCCPCPAPELLGGPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
DB      1 DKHTCCPCPAPELLGGPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 60

US-10-403-676-54
; Sequence 54, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRoche, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/423,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 54
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-676-54

Query Match      56.6%; Score 1271.5; DB 15; Length 878;
Best Local Similarity 63.8%; Pred. No. 2.4e-78;
Matches 271; Conservative 23; Mismatches 50; Indels 81; Gaps 16;

QY      2 DKHTCCPCPAPELLGGPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
DB      1 DKHTCCPCPAPELLGGPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 60
```

```
QY      62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKISKAK 121
DB      61 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKISKAK 120

QY      122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 181
DB      121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 180

QY      182 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK-----ETFPK 234
DB      181 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGKGGGGGGGFPB- 239

QY      235 YLHYDEE---TSHQLLCKDKCPGTYLKQH-----CTAKWK-----TVC 269
DB      240 -----DSEFISISH-----GNITQYPVFVGHKPGRNTTQRLHLDIQIMIMNGTLY 286

QY      270 APCPDHYT---DSWHTSDECLYCPVCKELQYVQECNRTHNRVCECK-EGRYLE---- 321
DB      287 IAARDHIYTVDTIDTSHTEE--LYCS---KLTWKSROAD-----VDTCRMKGKHDECHN 336

QY      322 IEFCLKHSRCPGPGVVOAGTPERTVCKRC-----PDGFFSNETSCKAPC---RKHT 371
DB      337 FIKVLLKND---DALFVCGTNAFNPSCRNYKMDTLEP---FGDEFSGMARCPYDAKHA 389

QY      372 NCSVP 376
DB      390 NVALP 394

RESULT 6
US-09-825-012-46
; Sequence 46, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-46

Query Match      55.6%; Score 1249; DB 9; Length 731;
Best Local Similarity 65.6%; Pred. No. 6.8e-77;
Matches 254; Conservative 15; Mismatches 56; Indels 62; Gaps 6;

QY      2 DKHTCCPCPAPELLGGPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
DB      241 DKHTCCPCPAPELLGGPSVFLPPPKDMLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 300

QY      62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKISKAK 121
DB      301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETKISKAK 360

QY      122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 181
DB      361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDL 420

QY      182 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK-----ETFPK 241
DB      421 DGSFFLYSKLTVDKSRWQOGNVFSCSMHEALHNHYTQKSLSLSPGKGGGGGGGFPB- 480
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QY 242 TSHQLLCKPCPGTYLKQ-----HCTAKWK---TVCAPCPDHYH-1----- 277
Db 481 TFGETKMSNATLVSYIVQILSRDYIALVQVRDLSHTAVGKLLDNLNQDAPDTYHYVWSE 540
QY 278 -----TDSWHTSDECLYCSPVKELQYVQKQECNRTHNRVCECK 315
Db 541 PLGRNSYKERYLFVVRPDQVSAVDSYYDDGCEPCG-----NDTFNREPAIV 587
QY 316 E--GRYLEI-EFCLKXRSPPGFGVVQ 339
Db 588 RFFSRFTEVREPAIVPLHAAPGDAVAE 614

RESULT 7
US-09-825-012-55
; Sequence 55, Application US/09825012
; Patent No. US2002012798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMEG1 heavy chain - DNase I fusion
US-09-825-012-55

Query Match 55.6%; Score 1249; DB 9; Length 741;
Best Local Similarity 65.6%; Pred. No. 6.9e-77;
Matches 254; Conservative 15; Mismatches 56; Indels 62; Gaps 6;

QY 2 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPETVTCVVDVSHEDDPVKFNWYVD 61
Db 241 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPETVTCVVDVSHEDDPVKFNWYVD 300
QY 62 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAK 121
Db 301 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAK 360
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 181
Db 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 420
QY 182 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPPVLD 241
Db 421 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPPVLD 480
QY 242 TSHQLLCKPCPGTYLKQ-----HCTAKWK---TVCAPCPDHYH-1----- 277
Db 481 TFGETKMSNATLVSYIVQILSRDYIALVQVRDLSHTAVGKLLDNLNQDAPDTYHYVWSE 540
QY 278 -----TDSWHTSDECLYCSPVKELQYVQKQECNRTHNRVCECK 315
Db 541 PLGRNSYKERYLFVVRPDQVSAVDSYYDDGCEPCG-----NDTFNREPAIV 587
QY 316 E--GRYLEI-EFCLKXRSPPGFGVVQ 339
Db 588 RFFSRFTEVREPAIVPLHAAPGDAVAE 614
```

## RESULT 8

US-10-385-802-44

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; Sequence 44, Application US/10385802
; Publication No. US20030224991A1
; GENERAL INFORMATION:
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: LaRoche, William J.
; APPLICANT: Lichenstein, Henri
; APPLICANT: Wu, Frank
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND AMINO ACID SEQUENCES OF
; FILE REFERENCE: 15966-517UB
; CURRENT APPLICATION NUMBER: US/10/385,802
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/363,266
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 44
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-385-802-44

Query Match 55.3%; Score 1241; DB 15; Length 489;
Best Local Similarity 85.5%; Pred. No. 1.5e-76;
Matches 236; Conservative 4; Mismatches 14; Indels 22; Gaps 2;

QY 2 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPETVTCVVDVSHEDDPVKFNWYVD 61
Db 1 DKHTCCPPCAPPELLGGPSVFLFPPPKDQTLMSRTPETVTCVVDVSHEDDPVKFNWYVD 60
QY 62 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAK 121
Db 61 GVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAK 120
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 181
Db 121 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 180
QY 182 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPPVLD 228
Db 181 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGKTTTPPVLD 240
QY 229 -----ETPPKYLHYDEETSHQLLCKPCPGTYLKQ 259
Db 241 PGYPRDLMPPP-----DLATSPKSPFKIPPVTFINE 272

RESULT 9
US-10-609-217-1056
; Sequence 1056, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: PEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-609-217-1056
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Query Match      55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGKETFPFKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGKETFPFKYLHYDE 240
QY 241 ETS 243
DB 241 NTS 243

RESULT 10
US-10-632-388-1056
; Sequence 1056, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNP-ALPA INHIBITORS
US-10-632-388-1056

Query Match      55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGKETFPFKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGKETFPFKYLHYDE 240
QY 241 ETS 243
DB 241 NTS 243

RESULT 11
US-10-651-723-1056
; Sequence 1056, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNP-ALPA INHIBITORS
US-10-651-723-1056

Query Match      55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHCTPCPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTPREEQYNSTRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGEVHNNAKTPREEQYNSTRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGKETFPFKYLHYDE 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGKETFPFKYLHYDE 240
QY 241 ETS 243
DB 241 NTS 243

RESULT 12
US-10-645-761-1056
; Sequence 1056, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
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; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-645-761-1056

Query Match          55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 13
US-10-666-696-1056
; Sequence 1056, Application US/1066696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-666-696-1056

Query Match          55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 14
US-10-653-048-1056
; Sequence 1056, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-653-048-1056

Query Match          55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 15
US-09-847-712-2
; Sequence 2, Application US/09847712
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QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 14
US-10-653-048-1056
; Sequence 1056, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPHA INHIBITORS
US-10-653-048-1056

Query Match          55.2%; Score 1240; DB 15; Length 248;
Best Local Similarity 95.1%; Pred. No. 8.3e-77;
Matches 231; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCAPPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGKGGGDFLPHYK 240

QY 241 ETS 243
DB 241 NTS 243

RESULT 15
US-09-847-712-2
; Sequence 2, Application US/09847712
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; Patent No. US20020090646A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: MARSHALL, WILLIAM S.  
; APPLICANT: REYNOLDS, ANGELA  
; TITLE OF INVENTION: CALCITONIN-RELATED MOLECULES  
; FILE REFERENCE: A-684  
; CURRENT APPLICATION NUMBER: US/09/847,712  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,511  
; PRIOR FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-712-2

Query Match 55.1%; Score 1238; DB 9; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1e-76;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDKHTCPCPAPELGGPSVFLFPKPKDTLMISPTPEVTCVWVDVSHEDPEVKFNWYV 60  
DB 1 MDKHTCPCPAPELGGPSVFLFPKPKDTLMISPTPEVTCVWVDVSHEDPEVKFNWYV 60  
QY 61 DGVVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
DB 61 DGVVHNATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120  
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180  
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNHYTOKLSLSFGK 228  
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNHYTOKLSLSFGK 228

Search completed: March 8, 2005, 15:16:17  
Job time : 61.5885 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 14:20:42 ; Search time 16.3429 Seconds  
(without alignments)  
2360.831 Million cell updates/sec

Title: US-09-389-782a-8  
Perfect score: 2246  
Sequence: 1 MKTHTCPPCPAPPELLGGPS.....QKGNATHDNCISGSESTOK 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 791.\*  
1: Pirl.\*  
2: Pirl.\*  
3: Pirl.\*  
4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	54.9	255	4	Ig gamma-1 chain C
2	1233	54.9	330	1	Ig gamma-1 chain C
3	1227	54.6	374	2	Ig heavy chain V r
4	1180	52.5	234	2	Ig gamma chain C r
5	1146	51.0	377	2	Ig gamma-3 chain C
6	1144	50.9	377	2	Ig gamma-3 chain C
7	1142.5	50.9	326	1	Ig gamma-2 chain C
8	1135	50.5	327	1	Ig gamma-4 chain C
9	1121	49.9	289	1	Ig gamma-3 heavy C
10	918.5	40.9	323	1	Ig gamma chain C r
11	906.5	40.4	328	2	Ig gamma 2b chain
12	906.5	40.4	328	2	Ig gamma 2a chain
13	903.5	40.2	277	2	Ig gamma 4 chain C
14	889	39.6	329	1	Ig gamma-2 chain C
15	885.5	39.4	328	2	Ig gamma 1 chain c
16	878.5	39.1	328	2	Ig gamma 3 chain c
17	855.5	38.1	470	2	Ig heavy chain pre
18	846	37.7	308	2	Ig heavy chain C r
19	846	37.7	472	2	Ig gamma-1 chain -
20	845.5	37.6	329	1	Ig gamma-3 chain C
21	838	37.3	333	2	Ig gamma-2b chain
22	835.5	37.2	338	1	Ig gamma-3 chain C
23	827.5	36.8	444	2	monoclonal antibod
24	818.5	36.4	326	2	Ig gamma-1 chain C
25	817.5	36.4	324	1	Ig gamma-1 chain C
26	812.5	36.2	393	1	Ig gamma-1 chain C
27	809.5	36.0	329	2	Ig gamma-2c chain
28	809	36.0	330	1	Ig gamma-2a chain
29	809	36.0	469	2	Ig gamma-2a chain

30	804	35.8	399	1	G2MSAM	Ig gamma-2a chain
31	802	35.7	335	1	G2MSAB	Ig gamma-2a chain
32	794	35.4	446	2	S40295	Ig gamma-2a chain
33	785.5	35.0	322	2	PS0019	Ig gamma-2a chain
34	779	34.7	474	1	G2MS11	Ig gamma-2b chain
35	774	34.5	405	1	G2MSBM	Ig gamma-2b chain
36	764	34.0	327	2	S06611	Ig gamma-2 chain C
37	757	33.7	475	2	S01321	Ig gamma-2b chain
38	707	31.5	180	2	I46732	Ig gamma heavy chain
39	577.5	25.7	249	2	S69340	Ig heavy chain V-I
40	574.5	25.6	218	2	A36040	Ig heavy chain V-I
41	571	25.4	152	2	S14236	Ig gamma-1 chain C
42	395.5	17.6	572	2	B4529	Ig Y heavy chain (
43	362	16.1	343	2	S25644	Ig mu chain C regi
44	362	16.1	453	2	S27768	Ig mu chain C regi
45	361	16.1	455	1	MHMS	Ig mu chain C regi

ALIGNMENTS

RESULT 1

S31866  
Ig gamma-1 chain C region - synthetic  
C/Species: synthetic  
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C/Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C/Accession: S31866  
R/Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A/Description: Screening method for protein-protein interactions of cloned gene products.  
A/Reference number: S31866  
A/Accession: S31866  
A/Molecule type: mRNA  
A/Residues: 1-255 -FILL>  
A/Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069  
C/Keywords: immunoglobulin  
F;1-22/Region: Escherichia coli outer membrane protein A precursor  
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 54.9%; Score 1233; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 4.2e-71;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	DKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	61
DB	29	DKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	88
QY	62	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	121
DB	89	GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	148
QY	122	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	181
DB	149	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD	208
QY	182	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK	228
DB	209	DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK	255

RESULT 2

GHU  
Ig gamma-1 chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
C/Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146  
R/Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.  
A/Reference number: A93433; UID:82274238; PMID:6287432  
A/Accession: A93433  
A/Molecule type: DNA

A;Residues: 1-330 <ELL>  
A;Cross-references: UNIPROT:P01857; EMBL:Z17370  
A;Note: this sequence has the GIm(17) allotypic marker, 97-Lys, and the GIm(1) markers,  
R;Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S33904  
A;Accession: S36861  
A;Molecule type: DNA  
A;Residues: 2-330 <HAR>  
A;Cross-references: EMBL:Z17370  
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A;Reference number: S33887; MUID:83001943; PMID:6811139  
A;Accession: S33887  
A;Molecule type: DNA  
A;Residues: 88-113,235-330 <TAK>  
A;Cross-references: EMBL:Z17370  
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
Biochemistry 9, 3161-3170, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A;Reference number: A90563; MUID:71064024; PMID:5489771  
A;Contents: myeloma protein Eu  
A;Accession: B90563  
A;Molecule type: protein  
A;Residues: 1-96,'R',98-135 <CUN>  
A;Note: this sequence has the GIm(3) marker, 97-Arg  
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A;Reference number: A90564; MUID:71064025; PMID:5530842  
A;Contents: Eu  
A;Accession: A90564  
A;Molecule type: protein  
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,  
A;Note: this sequence has the GIm(non-1) markers, 239-Glu and 241-Met  
R;Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668  
A;Molecule type: protein  
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
A;Note: this sequence has the GIm(17) and GIm(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KOI; disulfide bonds  
A;Accession: A91723  
A;Molecule type: protein  
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'N',242-266,'D',268-271,'D',273-330 <SCH  
A;Note: this sequence has the GIm(3) and GIm(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enamide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1002129  
A;Contents: annotation; disulfide bonds  
C;Genetics:  
A;Gene: GDB:120085  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 114/1; 224/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;137-206/Domain: immunoglobulin homology <IM2>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-103,144-204,250-308/Disulfide bonds: #status experimental  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 54.9%; Score 1233; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 5.5e-71;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
DB 104 DKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163  
QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
DB 164 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223  
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181  
DB 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 283  
QY 182 DGSFFLYSKLTVDKSRWQQGNVFCFSVNHAEALHNHYTQKSLSLSPGK 228  
DB 284 DGSFFLYSKLTVDKSRWQQGNVFCFSVNHAEALHNHYTQKSLSLSPGK 330  
RESULT 3  
S69339  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C;Accession: S69339; S72664  
R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogné, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A;Reference number: S69339; MUID:95262687; PMID:7744049  
A;Accession: S69339  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <KHA>  
A;Cross-references: EMBL:X81695  
R;Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S72664  
A;Accession: S72664  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140,'C',142-374 <KH2>  
A;Cross-references: EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
Query Match 54.68%; Score 1227; DB 2; Length 374;  
Best Local Similarity 99.1%; Pred. No. 1.5e-70;  
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
DB 148 DKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 207  
QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
DB 208 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267  
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181  
DB 268 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 327

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QY 182 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 228
Db 328 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 374

RESULT 4
PT0207
IG gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 52.5%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 8.5e-68;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 15 DTHTTCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74

QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 75 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 194

QY 182 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKS 221
Db 195 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKS 234

RESULT 5
A23511
IG gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
C;Genetics:
A;Gene: IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 51.0%; Score 1146; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 2e-65;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 151 DTPTPCRCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

RESULT 6
A60764
IG gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 50.9%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 2.7e-65;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 151 DTPTPCRCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 211 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 270

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 330

QY 182 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 228
Db 331 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 377

RESULT 7
G2HU
IG gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PJ
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi
A;Reference number: A92809; MUID:81007873; PMID:6774012

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QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 211 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 270

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 330

QY 182 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 228
Db 331 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 377

```

## RESULT 6

```

A60764
IG gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

```

Query Match 50.9%; Score 1144; DB 2; Length 377;

Best Local Similarity 92.5%; Pred. No. 2.7e-65;

Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61

Db 151 DTPTPCRCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121

Db 211 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 270

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181

Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 330

QY 182 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 228

Db 331 DGSFFLYSKLTVDKSRWQGNVPSVMSVHEALHNHYTQKSLSPGK 377

## RESULT 7

G2HU

IG gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PJ

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi

A;Reference number: A92809; MUID:81007873; PMID:6774012

A:Contents: myeloma protein Til  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-  
A:Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin S  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4940472  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69054124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 50.9%; Score 1142.5; DB 1; Length 326;  
Best Local Similarity 94.1%; Pred. No. 2.9e-65;  
Matches 209; Conservative 8; Mismatches 4; Indels 1; Gaps 1;  
QY 7 CPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66  
DB 106 CPPCPAPP-VAGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 164  
QY 67 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126  
DB 165 NAKTKPREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPRE 224  
QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 186  
DB 225 PQVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 284  
QY 187 LYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 228  
DB 285 LYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 326

## RESULT 8

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 &lt;ELL&gt;

A:Cross-references: UNIPROT:P01861

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 &lt;PIN&gt;

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1, 111/1, 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology &lt;IM1&gt;

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology &lt;IM2&gt;

F:240-307/Domain: immunoglobulin homology &lt;IM3&gt;

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.5%; Score 1135; DB 1; Length 327;

Best Local Similarity 93.7%; Pred. No. 8.6e-65;

Matches 208; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 7 CPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66

DB 106 CPPCPAPEFLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 165

QY 67 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126

DB 166 NAKTKPREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPRE 225

QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 186

DB 226 PQVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 285

QY 187 LYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 228

DB 286 LYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 327

## RESULT 9

G3HUW1

Ig gamma-3 heavy chain disease proteins - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1979 #sequence revision 23-Oct-1981 #text\_change 16-Jul-1999

C:Accession: A90442; A92219; A90198; A93915; A02149

R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-&lt;

A:Reference number: A90442; MUID:81021548; PMID:6774747

A:Contents: heavy-chain disease protein Wis  
 A:Accession: A90442  
 A:Molecule type: protein  
 A:Residues: 1-289 <FRA>  
 A>Note: this molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain residue in the V region and all of the CH1 region. Residue 12 corresponds to the sequence of residues 42-76 was taken from the reference that follows  
 R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.  
 J. Biol. Chem. 252, 883-889, 1977  
 A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of the amino acid sequence of the heavy chain disease protein  
 A:Reference number: A92219; MUID:77118561; PMID:402363  
 A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
 A:Accession: A92219  
 A:Molecule type: protein  
 A:Residues: 12-97 <MIC>  
 A>Note: the hinge region in gamma-3 chains is about four times as long as in other gamma chain segments (12-28)  
 R:Wolfeinstein-Tudel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.  
 Biochem. Biophys. Res. Commun. 71, 907-914, 1976  
 A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the amino acid sequence of the heavy chain disease protein  
 A:Reference number: A90198; MUID:77021516; PMID:823945  
 A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues 12-97  
 A:Accession: A90198  
 A:Molecule type: protein  
 A:Residues: 59-125, 'E', 128-226, 228-289 <WOL>  
 A>Note: this protein lacks most of the V region, all of the CH1 region, and part of the CH2 region  
 R:Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
 A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion  
 A:Reference number: A93915; MUID:82247835; PMID:6808505  
 A:Contents: heavy chain disease protein Om  
 A:Accession: A93915  
 A:Molecule type: mRNA  
 A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
 A>Note: a carboxyl-terminal Lys is removed posttranslationally  
 A:Note: this sequence may represent an allelic form or another gamma chain subclass  
 C:Comment: The heavy chain disease protein Wis is shown.  
 C:Genetics:  
 A:Gene: GDB:119339; OMIM:147120  
 A:Cross-references: GDB:119339; OMIM:147120  
 A:Map position: 14q32.33-14q32.33  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid  
 F;203-270/Domain: immunoglobulin homology <IMM>  
 F;1/Modified site: pyroglutamic acid (Gln) #status experimental  
 F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 Query Match 49.9%; Score 1121; DB 1; Length 289;  
 Best Local Similarity 90.3%; Pred. No. 5.8e-64;  
 Matches 204; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 QY 2 DKTHCPAPALGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENYVD 61  
 DB 64 DTPPPCPAPALGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKENYVD 123  
 QY 62 GVEVHNKTPREQNSTYRVVSVLTVLHQLDGLNGKEYKCKVSNKALPAPIETKISKAK 121  
 DB 124 GVQVHNKTPREQNSTYRVVSVLTVLHQLDGLNGKEYKCKVSNKALPAPIETKISKAK 183  
 QY 122 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLS 181  
 DB 184 GQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLS 243  
 QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPG 227  
 DB 244 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPG 289  
 RESULT 10  
 GHRB  
 Ig gamma chain C region - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004  
 C:Accession: A91749; A90290; A93928; A90245; A94416; A02161  
 R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
 Immunogenetics 18, 387-397, 1983  
 A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype  
 A:Reference number: A91749; MUID:84030930; PMID:61313520  
 A:Accession: A91749  
 A:Molecule type: mRNA  
 A:Residues: 1-323 <BER>  
 A:Cross-references: UNIPROT:P01870  
 A>Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
 R:Pratt, D.M.; Mole, L.E.  
 Biochem. J. 151, 337-349, 1975  
 A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G  
 A:Reference number: A90290; MUID:76135469; PMID:1243651  
 A:Accession: A90290  
 A:Molecule type: protein  
 A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>  
 R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
 A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
 A:Reference number: A93928; MUID:83299917; PMID:6193512  
 A:Accession: A93928  
 A:Molecule type: mRNA  
 A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
 A:Cross-references: GDB:119339; OMIM:147120  
 A:Note: this sequence has the d12 allotypic marker, 104-Met, and the e15 allotypic marker  
 R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
 Biochem. J. 116, 249-259, 1970  
 A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G  
 A:Reference number: A90245; MUID:70110015; PMID:5461106  
 A:Accession: A90245  
 A:Molecule type: protein  
 A:Residues: 132-143, 'E', 145-161 <FRU>  
 R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
 In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, 1970  
 A:Reference number: A94416  
 A:Accession: A94416  
 A:Molecule type: protein  
 A:Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', 233-244  
 A:Note: this has the e15 allotypic marker, 185-Ala  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;20-82/Domain: immunoglobulin homology <IM1>  
 F;130-199/Domain: immunoglobulin homology <IM2>  
 F;236-303/Domain: immunoglobulin homology <IM3>  
 F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 40.9%; Score 918.5; DB 1; Length 323;  
 Best Local Similarity 71.7%; Pred. No. 4.2e-51;  
 Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;  
 QY 1 MDKT---HTC--PPCPAPALGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVK 55  
 DB 91 VDKTVAPSTCKPTCPPELPGSPVFIPPPKPTLMISRTPEVTCVVVDVSHEDPEVK 150  
 QY 56 FNNYDGVGVHNAKTPREQNSTYRVVSVLTVLHQLDGLNGKEYKCKVSNKALPAPIEK 115  
 DB 151 FTWYINNEQVTRAPPLRPPLEQQNSTYRVVSVLTPIHQLDGLNGKEYKCKVSNKALPAPIEK 210  
 QY 116 TISKAGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 175  
 DB 211 TISKAGQPLEPKVYTMGPPRELSRSVSLTCMNGFYPSDISVEWENKGAEDNYKT 270  
 QY 176 PPVLSDSGFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPG 228  
 DB 271 PAVLSDSGSYFLYKLSVPTSEWQSGDVFTCSVMHEALHNHYTQKSISRSPG 323  
 RESULT 11  
 147160

Ig gamma 2b chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47160  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126  
C:Genetics:  
A:Gene: IgG2b  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 40.4%; Score 906.5; DB 2; Length 328;  
Best Local Similarity 73.2%; Pred. No. 2.4e-50;  
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 7 CPCCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66  
DB 106 CPICPACE-SPGSPVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164  
QY 67 NAKTKPREQYNSTYRVSVLTPLHODWLNGKEYCKVSNKALPAPIETKISKAKGQPRE 126  
DB 165 TAQTRPKEQFNSTYRVSVLTPLHODWLNGKEYCKVSNKALPAPIETKISKAKGQPRE 224  
QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGS 184  
DB 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEQWQNGQPEPEGNRTTTPPQDQVDGT 284  
QY 185 FFLYSKLTVDKSRWQGNVFCVSMHEALHNYHTQKSLSPGK 228  
DB 285 YFLYSKFSVDKASQWGGIFQCAVMEALHNYHTQKSLSPGK 328

RESULT 12  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124  
C:Genetics:  
A:Gene: IgG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 40.4%; Score 906.5; DB 2; Length 328;  
Best Local Similarity 73.2%; Pred. No. 2.4e-50;  
Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 7 CPCCPAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 66  
DB 106 CPICPACE-SPGSPVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164  
QY 67 NAKTKPREQYNSTYRVSVLTPLHODWLNGKEYCKVSNKALPAPIETKISKAKGQPRE 126  
DB 165 TAQTRPKEQFNSTYRVSVLTPLHODWLNGKEYCKVSNKALPAPIETKISKAKGQPRE 224  
QY 127 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGS 184

DB 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEQWQNGQPEPEGNRTTTPPQDQVDGT 284  
QY 185 FFLYSKLTVDKSRWQGNVFCVSMHEALHNYHTQKSLSPGK 228  
DB 285 YFLYSKFSVDKASQWGGIFQCAVMEALHNYHTQKSLSPGK 328

RESULT 13  
I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47162  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47162  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <KAC>  
A:Cross-references: EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PID:G433130  
C:Genetics:  
A:Gene: IgG4  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 903.5; DB 2; Length 277;  
Best Local Similarity 71.1%; Pred. No. 3.1e-50;  
Matches 167; Conservative 30; Mismatches 31; Indels 7; Gaps 4;

QY 1 MDK---THTCPPCP-APELLG-GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55  
DB 43 VDKRVGVTKEPCPCACEGPGPSAFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 102  
QY 56 PNWYDGVGVNNAKTPREQYNSTYRVSVLTPLHODWLNGKEYCKVSNKALPAPIETK 115  
DB 103 FSWYVDGVGVHTAQRPEQFNSTYRVSVLTPLHODWLNGKEYCKVSNKALPAPIETK 162  
QY 116 TISKAGQPREQYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYK 173  
DB 163 IISKAGQTRFPQYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYK 222  
QY 174 TTPPVLSDSGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNYHTQKSLSPGK 228  
DB 223 TTPPQDQVDGTYFLYSKLVADKASQWQGDITFQCAVMEALHNYHTQKSLSPGK 277

RESULT 14  
GZGP  
Ig gamma-2 chain C region - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C>Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004  
C:Accession: A94553; A90352; A90359; A90384; A90385; A02151  
R:Trischmann, T.M.  
submitted to the Atlas, April 1975  
A:Reference number: A94553  
A:Accession: A94553  
A:Molecule type: protein  
A:Residues: 1-3 <TRI>  
A:Cross-references: UNIPROT:P01862  
R:Birstein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
A:Reference number: A90352; MUID:71058471; PMID:538606  
A:Accession: A90352  
A:Molecule type: protein  
A:Residues: 4-68 <BIR>  
R:Turner, K.J.; Cebra, J.J.  
Biochemistry 10, 9-17, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir  
A:Reference number: A90359; MUID:71058486; PMID:538616  
A:Accession: A90359

A:Molecule type: protein  
A:Residues: 69-133,312-329 <TR>  
R:Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90384; MUID:75036072; PMID:4429665  
A:Accession: A90384  
A:Molecule type: protein  
A:Residues: 134-226 <TRA>  
R:Trichmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90385; MUID:75036073; PMID:4609467  
A:Accession: A90385  
A:Molecule type: protein  
A:Residues: 227-311 <TR2>  
R:Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
A:Reference number: A90354; MUID:71058474; PMID:4922544  
A:Contents: annotation; disulfide bonds  
A:Note: Cys-16 is involved in a heavy-light chain bond  
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:21-81/Domain: immunoglobulin homology <IM1>  
F:135-204/Domain: immunoglobulin homology <IM2>  
F:241-310/Domain: immunoglobulin homology <IM3>  
F:28-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Asn) (covalent)  
F:248-308/Disulfide bonds: #status experimental

Query Match 39.6%; Score 889; DB 1; Length 329;  
Best Local Similarity 72.3%; Pred. No. 3.1e-49;  
Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;  
QY 6 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65  
DB 106 TCEKCPPENLGGPSVFIAPPKPKDTLMISLPRVTCVVVDVSDQDEPEVQFTWFDNKPV 165  
QY 66 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125  
DB 166 GNAETKPRVEQNTTFRVESVLPVQHODWLGKGEKCKVSNKALPAPIEKTISKAKGAPR 225  
QY 126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDSDG 183  
DB 226 MPDVYTLPPSRDELTKSKSVTCLIIINFPADIHVEWASNRVFSKEYKNTPTPIEDADG 285  
QY 184 SFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG 227  
DB 286 SYFLYSKLTVDKSAWDQGVITTCVSNVHEALHNHYTQKALSRSFG 329

RESULT 15  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47158  
A:Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03778; NID:g4333121; PIDN:AAA52216.1; PID:g4333122  
C:Genetic:

A:Gene: IgG1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMW>  
Query Match 39.4%; Score 885.5; DB 2; Length 328;  
Best Local Similarity 72.4%; Pred. No. 5.2e-49;  
Matches 163; Conservative 27; Mismatches 32; Indels 3; Gaps 2;  
QY 6 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65  
DB 105 TCPICPGCE-VAGPSVFIPPPKPKDTLMISQTPETCVVVDVSKHAHVQFSWYVDGVEV 163  
QY 66 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125  
DB 164 HTAETRPKEEQNSTYRVVSVLPVQHODWLGKGEKCKVSNVVDLPAPITRTISKALGQSR 223  
QY 126 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--PENNYKTTTPPVLDSDG 183  
DB 224 EPQVYTLPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTTPPQDDVDG 283  
QY 184 SFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228  
DB 284 TFFLYSKLAVDKARWDHGDGKPECAVMHEALHNHYTQKSISTQGGK 328

Search completed: March 8, 2005, 14:46:15  
Job time : 16.3429 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 14:19:56 ; Search time 74.1412 Seconds  
(without alignments)  
2769.633 Million cell updates/sec

Title: US-09-389-782A-8

Perfect score: 2246

Sequence: 1 MKTHTCPCPAPPELLGGPS.....QKGNATHDNCISGSESTOK 401

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1233	54.9	330	1	GCL_HUMAN	P01857 homo sapien
2	1233	54.9	465	2	Q6GMX6	Q6gm66 homo sapien
3	1233	54.9	466	2	Q6IN78	Q6in78 homo sapien
4	1233	54.9	469	2	Q7Z7P5	Q7z7p5 homo sapien
5	1233	54.9	470	2	Q6PJA4	Q6pj44 homo sapien
6	1233	54.9	470	2	Q6PJA4	Q6pj44 homo sapien
7	1233	54.9	472	2	Q6N089	Q6n089 homo sapien
8	1233	54.9	475	2	Q6GMW7	Q6gmw7 homo sapien
9	1233	54.9	476	2	Q6GMX1	Q6gm61 homo sapien
10	1233	54.9	679	2	Q96PQ8	Q96pq8 homo sapien
11	1229	54.7	473	2	Q6P055	Q6p055 homo sapien
12	1229	54.7	475	2	Q6M2Q6	Q6m2q6 homo sapien
13	1229	54.7	480	2	Q6N094	Q6n094 homo sapien
14	1229	54.7	481	2	Q6N097	Q6n097 homo sapien
15	1229	54.7	482	2	Q7Z351	Q7z351 homo sapien
16	1227	54.6	348	2	Q6PYX1	Q6pyx1 homo sapien
17	1227	54.6	473	2	Q6M2V7	Q6m2v7 homo sapien
18	1227	54.6	478	2	Q6P181	Q6p181 homo sapien
19	1227	54.6	480	2	Q6P1F1	Q6p1f1 homo sapien
20	1226	54.6	466	2	Q6N096	Q6n096 homo sapien
21	1222	54.4	475	2	Q6N095	Q6n095 homo sapien
22	1222	54.4	544	2	Q6P095	Q6p095 homo sapien
23	1216	54.1	487	2	Q652L2	Q652l2 mus sp. fv/
24	1146	51.0	354	2	Q86T22	Q86tt2 homo sapien
25	1146	51.0	518	2	Q6N030	Q6n030 homo sapien
26	1142.5	50.9	326	1	GCL_HUMAN	P01859 homo sapien
27	1142.5	50.9	417	2	Q6N093	Q6n093 homo sapien
28	1142	50.8	521	2	Q8N4Y9	Q8n4y9 homo sapien
29	1139.5	50.7	464	2	Q6M2U6	Q6m2u6 homo sapien
30	1137.5	50.6	465	2	Q6P6C4	Q6p6c4 homo sapien
31	1135	50.5	327	1	GCL_HUMAN	P01861 homo sapien

#### RESULT 1

ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Edlison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079 (1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RN	[5]			
RP	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).			
RX	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RA	MEDLINE=83289131; PubMed=6884994;			
RT	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RL	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RN	[6]			
RP	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).			
RX	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			

32	1135	50.5	473	2	Q8TC63	Q8tc63 homo sapien
33	1131	50.4	509	2	Q8NF17	Q8nf17 homo sapien
34	1128.5	50.2	493	2	Q68CN4	Q68cn4 homo sapien
35	1126	50.1	290	1	GC3_HUMAN	P01860 homo sapien
36	1126	50.1	476	2	Q6MZX7	Q6mzx7 homo sapien
37	1009	44.9	401	1	T11B_HUMAN	O00300 homo sapien
38	918.5	40.9	323	1	GC_RABIT	P01870 oryctolagus
39	909	40.5	337	2	Q95W34	Q95w34 equus caball
40	892	39.7	401	2	Q6P112	Q6p112 mus musculus
41	889	39.6	329	1	GC2_CAVPO	P01862 cavia porce
42	888	39.5	401	1	T11B_MOUSE	O08712 mus musculus
43	875	39.0	401	1	T11B_RAT	O08727 rattus norv
44	845.5	37.6	329	1	GC3_MOUSE	P22436 mus musculus
45	845.5	37.6	470	2	Q7TNK1	Q7tnk1 mus musculus

#### ALIGNMENTS



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QY 62 GVEVHNKTPREEQNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIKTIKAK 121
DB 164 GVEVHNKTPREEQNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIKTIKAK 223
QY 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
DB 224 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 283
QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 284 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

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Query Match 54.9%; Score 1233; DB 2; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-73;

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Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTHTCCPAPBELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 239 DKHTHTCCPAPBELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 298
QY 62 GVEVHNKTPREEQNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIKTIKAK 121
DB 299 GVEVHNKTPREEQNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIKTIKAK 358
QY 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 181
DB 359 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 418
QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 419 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 465

RESULT 3
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.

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DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDB81076E CRC64;

Query Match 54.9%; Score 1233; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 6.8e-73;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTCPAPALGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 240 DKHTCTCPAPALGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 299
QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
DB 300 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 359
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 360 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 419
QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 420 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 466

RESULT 4
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS00835; IG LIKE; 4.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 54.9%; Score 1233; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 6.8e-73;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTCPAPALGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 243 DKHTCTCPAPALGGPSVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 302
QY 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
DB 303 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 362
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
DB 363 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 422
QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 423 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 469

RESULT 5
Q6PJ44 PRELIMINARY; PRT; 470 AA.
AC Q6PJ44
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.

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DR Pfam: PF07654; Cl-set; 3.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGC1; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR SMART: SM00835; IG LIKE; 4.  
 DR PROSITE: PS00835; IG\_MHC; UNKNOWN\_2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 DR KW Hypothetical protein.  
 DR SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;  
 Query Match 54.9%; Score 1233; DB 2; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-73;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61  
 DB 244 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 303  
 QY 62 GVEVHNKTKPREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAK 121  
 DB 304 GVEVHNKTKPREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAK 363  
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181  
 DB 364 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 423  
 QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228  
 DB 424 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
 RESULT 6  
 Q7Z5W1 PRELIMINARY; PRT; 470 AA.  
 AC Q7Z5W1;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vialalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Sklaska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC053984; AAH53984.1; -.  
 DR HSSP: P01857; 1HZH.

DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF07654; Cl-set; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 DR KW Hypothetical protein.  
 DR SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;  
 Query Match 54.9%; Score 1233; DB 2; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-73;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61  
 DB 244 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 303  
 QY 62 GVEVHNKTKPREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAK 121  
 DB 304 GVEVHNKTKPREEQNSTYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAK 363  
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181  
 DB 364 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 423  
 QY 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228  
 DB 424 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
 RESULT 7  
 Q6N089 PRELIMINARY; PRT; 472 AA.  
 AC Q6N089;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686P15220.  
 GN Name=DKFZp686P15220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RG The German Human CDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BX640627; CAE45781.1; -.  
 DR HSSP: P01861; 1ADQ.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF07654; Cl-set; 3.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGC1; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 DR KW Hypothetical protein.  
 DR SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;  
 Query Match 54.9%; Score 1233; DB 2; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-73;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61

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Db 246 DKHTCTPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 305
Qy 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 306 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 365
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 366 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 425
Qy 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 228
Db 426 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 472

RESULT 8
Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IGL1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1F55D736860F8 CRC64;
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Query Match 54.9%; Score 1233; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 6.9e-73;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DKHTCTPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
Db 249 DKHTCTPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308
Qy 62 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 309 GVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 428
Qy 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 228
Db 429 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 475

RESULT 9
Q6GMX1 PRELIMINARY; PRT; 476 AA.
ID Q6GMX1
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IGL1; 3.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABAS62DD89D CRC64;  
  
Query Match 54.9%; Score 1233; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 7e-73;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
DB 250 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 309  
QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
DB 310 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 369  
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181  
DB 370 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 429  
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228  
DB 430 DGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 476  
  
RESULT 10  
Q96PQ8 PRELIMINARY; PRT; 679 AA.  
AC Q96PQ8  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Factor VII active site mutant immunoconjugate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;  
RA Hu Z., Garen A.;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
cells for immunotherapy in mouse models of prostatic cancer."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hu Z., Garen A.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF272774; AAK58686.2; -.  
DR HSSP; P08709; 1KLI.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPRO00152; Asx hydroxyl\_s.  
DR InterPro; IPRO00742; EGF\_2.  
DR InterPro; IPRO01881; EGF\_Ca.  
DR InterPro; IPRO06209; EGF\_Like.  
DR InterPro; IPRO07110; Ig-like.  
DR InterPro; IPRO03597; Ig\_c1.  
DR InterPro; IPRO03006; Ig\_MHC.  
DR InterPro; IPRO01254; Peptidase s1.  
DR InterPro; IPRO09003; Pept Ser\_Cys.  
DR InterPro; IPRO00294; VitK\_dep\_GLA.  
DR Pfam; PF07654; C1-set; 2.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00594; Gla; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00407; IGC1; 1.

DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLA\_1; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE; PS00240; TRYPsin DOM; 1.  
DR PROSITE; PS00134; TRYPsin HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPsin SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;  
  
Query Match 54.9%; Score 1233; DB 2; Length 679;  
Best Local Similarity 100.0%; Pred. No. 1e-72;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
DB 453 DKHTCCPPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 512  
QY 62 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
DB 513 GVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 572  
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181  
DB 573 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 632  
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228  
DB 633 DGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 679  
  
RESULT 11  
Q6P055 PRELIMINARY; PRT; 473 AA.  
ID Q6P055  
AC Q6P055;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]



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QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 374 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 433
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 228
DB 434 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 480

RESULT 14
Q6N097 ID Q6N097 PRELIMINARY; PRT; 481 AA.
AC G6N097;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686H20196.
GN Names=DKFZp686H20196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640619; CAB45773.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 47220D9B64BDF98B CRC64;

Query Match 54.7%; Score 1229; DB 2; Length 481;
Best Local Similarity 99.6%; Pred. No. 1.3e-72;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 255 DKHTCCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 314
QY 62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 315 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 374
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 375 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 434
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 228
DB 435 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 481

RESULT 15
Q7Z351 ID Q7Z351 PRELIMINARY; PRT; 482 AA.
AC Q7Z351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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DE Hypothetical protein DKFZp686N02209.
GN Name=DKFZp686N02209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; IHZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 54.7%; Score 1229; DB 2; Length 482;
Best Local Similarity 99.6%; Pred. No. 1.3e-72;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 256 DKHTCCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 315
QY 62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 316 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 375
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
DB 376 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 435
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 228
DB 436 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 482

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Job time : 74.1412 secs
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